

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: Innogenetics sa.
- (B) STREET: Industriepark Zwijnaarde 7, box 4
- (C) CITY: Ghent
- (E) COUNTRY: Belgium
- (F) POSTAL CODE (ZIP): B-9052
- (G) TELEPHONE: 00 32 9 241 07 11
- (H) TELEFAX: 00 32 9 241 07 99

(ii) TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, prophylaxis and therapy.

(iii) NUMBER OF SEQUENCES: 270

## (iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: BR34-4-20

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG 48  
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
     1                    5                    10                    15

GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC 96  
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr

20 96 30  
25

AGC TTC GGT AAC ACA ATC ACT TGC TAC ATC AAG GCC ACA GCG GCT GCA 144  
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
35 40 45

AGG GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT 192  
Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
50 55 60

CTG GTC GTG GTG GCT GAG AGT 213  
Leu Val Val Val Ala Glu Ser  
65 70

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
35 40 45

Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
50 55 60

Leu Val Val Val Ala Glu Ser  
65 70

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: BR36-23-18

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTC ACG GAA CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG 48  
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15

GCC CAG TGT GGT TAT CGC CGC TGC CGT GCC AGT GGA GTT CTG CCT ACC 96  
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30

AGC TTC GGC AAC ACA ATC ACT TGC TAC ATC AAG GCC ACA GCG GCT GCA 144  
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45

AGG GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT 192  
 Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

CTG GTC GTG GTG GCT GAG AGT 213  
 Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45

Arg Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:  
(B) CLONE: BR36-23-18
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTC	ACG	GAG	CGG	CTT	TAC	TGC	GGG	GGC	CCT	ATG	TTT	AAC	AGC	AAG	GGG	48
Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10					15		
GCC	CAG	TGT	GGT	TAT	CGC	CGT	TGC	CGT	GCC	AGT	GGA	GTT	CTG	CCT	ACC	96
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
			20					25					30			
AGC	TTC	GGC	AAC	ACA	ATC	ACT	TGT	TAC	ATC	AAA	GCC	ACA	GCG	GCC	GCA	144
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
			35				40					45				
AAA	GCC	GCA	GGC	CTC	CGG	AGC	CCG	GAC	TTT	CTT	GTC	TGC	GGA	GAT	GAT	192
Lys	Ala	Ala	Gly	Leu	Arg	Ser	Pro	Asp	Phe	Leu	Val	Cys	Gly	Asp	Asp	
			50				55					60				
CTG	GTC	GTG	GTG	GCT	GAG	AGT										
Leu	Val	Val	Val	Ala	Glu	Ser										213
65							70									

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu	Thr	Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Phe	Asn	Ser	Lys	Gly	
1				5					10					15		
Ala	Gln	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Pro	Thr	
			20					25					30			
Ser	Phe	Gly	Asn	Thr	Ile	Thr	Cys	Tyr	Ile	Lys	Ala	Thr	Ala	Ala	Ala	
			35				40					45				



99

Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-23-20

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTT AAC AGC AAA GGG	43
Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly	
1 5 10 15	
GCC CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC	95
Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr	
20 25 30	
AGC TTC GGC AAC ACA ATC ACT TGT TAC ATC AAA GCC ACA GCG GCC GCA	144
Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala	
35 40 45	
AAA GCC GCA GGC CTC CGG AGC CCG GAC TTT CTT GTC TGC GGA GAT GAT	192
Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp	
50 55 60	
CTG GTC GTG GTG GCT GAG AGT	213
Leu Val Val Val Ala Glu Ser	
65 70	

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15  
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30  
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45  
 Lys Ala Ala Gly Leu Arg Ser Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60  
 Leu Val Val Val Ala Glu Ser  
 65 70

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-2-17

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG 48  
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15  
 GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC 96  
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30  
 AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA 144  
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45  
 AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT 192

101

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

TTG GTC GTG GTG GCT GAG AGT  
 Leu Val Val Val Ala Glu Ser  
 65 70

213

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: BR33-2-21

## (ix) FEATURE:

- (A) NAME/KEY: CDS -
- (B) LOCATION: 1..213

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTC ACG GAG CGG CTT TAC TGC GGG GGC CCT ATG TTC AAC AGC AAG GGG 48  
 Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15

GCC CAG TGT GGT TAT CGC CGT TGT CGT GCC AGT GGA GTT CTG CCT ACC 96  
 Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30

AGT TTC GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA GCG GCT GCA 144  
 Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45

AAA GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTT TGC GGA GAT GAT 192  
 Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

TTG GTC GTG GTG GCT GAG AGT 213  
 Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly  
 1 5 10 15

Ala Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr  
 20 25 30

Ser Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Ala Ala Ala  
 35 40 45

Lys Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp  
 50 55 60

Leu Val Val Val Ala Glu Ser  
 65 70

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-5

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATG TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA	526
Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser	
160 165 170 175	

GGA CAC CGA ATG GCT  
Gly His Arg Met Ala  
180

541

## (2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
65 70 75 80

Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
85 90 95

Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Met Leu Val Gly  
115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
165 170 175

His Arg Met Ala  
180

## (2) INFORMATION FOR SEQ ID NO: 15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09873324 060504  
T05090 42222860

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-3-14

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CCT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACA ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	
GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT	478
Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His	
145 150 155	
CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA	526

Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175

GGA CAC CGA ATG GCT  
 Gly His Arg Met Ala  
 180

541

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15  
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30  
 Cys Ser Phe Ser Ile Phe Leu Pro Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45  
 Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60  
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80  
 Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95  
 Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
 100 105 110  
 Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly  
 115 120 125  
 Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
 130 135 140  
 Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160  
 Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
 165 170 175  
 His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 17 :

## (i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 541 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: HD10-2-21

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

C GTC GGC GCT CCT GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAC ACG TCT GGC CTC TAC GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT CAG GAC GGT AAT	286
Val Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCT GCG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AGG TAC	334
Thr Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGG CAT GTA GAC ATA TTG GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val	
115 120 125	
GGC GCG GCC ACG ATG TGC TCT GCT CTC TAC GTG GGT GAT ATG TGT GGG	430
Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly	
130 135 140	

GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT 478  
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His  
 145 150 155

CAA ACG GTC CAG ACC TGT AAC TGC TCA CTG TAC CCA GGC CAT CTT TCA 526  
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175

GGA CAC CGA ATG GCT 541  
 Gly His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80

Ile Leu His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95

Ser Ala Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Arg His Val Asp Ile Leu Val Gly  
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
 165 170 175

His Arg Met Ala

180

## (2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 541 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-9-13

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	
GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG	382
Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val	
115 120 125	

GGC GCG GCC ACG ATG TGC TCA GCG CTC TAC GTG GGT GAT ATG TGT GGG 430  
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly  
 130 135 140

GCC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT 478  
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His  
 145 150 155

CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 526  
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175

GGA CAT CGA ATG GCT 541  
 Gly His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80

Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val  
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly  
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly

165

170

175

His Arg Met Ala  
180

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-9-20

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATT TTC CTT CTT GCT CTG TTC TCT TGC TTA ATT	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT AGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGC AGT ATT GTG TAC GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC ACA CCC GGC TGC ATA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	
ACA TCC ACG TGC TGG ACC CCA GTG ACA CCT ACA GTG GCA GTC AAG TAC	334
Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr	
100 105 110	

GTC GGA GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG 382  
 Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
                   115                  120                  125

GGC GCG GCC ACG ATG TGC TCT GCG CTC TAC GTG GGT GAC ATG TGT GGG 430  
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly  
                   130                  135                  140

GCT GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT CGT CGC CAT 478  
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His  
                   145                  150                  155

CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 526  
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
                   160                  165                  170                  175

GGA CAT CGA ATG GCT  
 Gly His Arg Met Ala 541  
                   180

## (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
   1                  5                  10                  15

Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
                   20                  25                  30

Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
                   35                  40                  45

Pro Ala Ala Ser Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
                   50                  55                  60

Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
                   65                  70                  75                  80

Ile Leu His Thr Pro Gly Cys Ile Pro Cys Val Gln Asp Gly Asn Thr  
                   85                  90                  95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Lys Tyr Val  
                   100                  105                  110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly  
                   115                  120                  125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
                   130                  135                  140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
 165 170 175

His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-10

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 2..541

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGT AGT AAT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	
GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT	286
Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn	
80 85 90 95	

ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC 334  
 Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr  
 100 105 110  
 GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA 382  
 Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
 115 120 125  
 GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG 430  
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly  
 130 135 140  
 GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT 478  
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His  
 145 150 155  
 CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 526  
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175  
 GGA CAT CGC ATG GCT 541  
 Gly His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15  
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30  
 Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45  
 Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60  
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80  
 Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95  
 Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
 100 105 110  
 Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly



115

120

125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
 165 170 175

His Arg Met Ala  
 180

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-19

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCT TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	
CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC	238
Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp	
65 70 75	

GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT 286  
 Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn  
 80 85 90 95  
 ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC 334  
 Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr  
 100 105 110  
 GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA 382  
 Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
 115 120 125  
 GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG 430  
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly  
 130 135 140  
 GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT 478  
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His  
 145 150 155  
 CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 526  
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175  
 GGA CAT CGA ATG GCT 541  
 Gly His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15  
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30  
 Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45  
 Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60  
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80  
 Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
 85 90 95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
 100 105 110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly  
 115 120 125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
 130 135 140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
 145 150 155 160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
 165 170 175

His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 541 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR33-1-20

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

C GTC GGC GCT CCC GTA GGA GGC GTC GCA AGA GCC CTT GCG CAT GGC	46
Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly	
1 5 10 15	
GTG AGG GCC CTT GAG GAC GGG ATA AAC TTC GCA ACA GGG AAT TTG CCC	94
Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro	
20 25 30	
GGT TGC TCT TTT TCT ATC TTC CTT CTT GCT CTG TTC TCT TGC TTA ATC	142
Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile	
35 40 45	
CAT CCA GCA GCT GGT CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC	190
His Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val	
50 55 60	

CTT ACC AAC GAC TGT TCC AAT AGT AGT ATT GTG TAT GAG GCC GAT GAC 238  
 Leu Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp  
 65 70 75  
 GTT ATT CTG CAC GCG CCC GGC TGT GTA CCT TGT GTC CAG GAC GGC AAT 286  
 Val Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn  
 80 85 90 95  
 ACG TCT ACA TGC TGG ACC CCA GTA ACA CCT ACA GTG GCA GTC AGG TAC 334  
 Thr Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr  
 100 105 110  
 GTC GGG GCA ACC ACC GCT TCG ATA CGC AGT CAT GTG GAC CTG TTA GTA 382  
 Val Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val  
 115 120 125  
 GGC GCG GCC ACG ATG TGC TCT GCG CTT TAC GTG GGT GAT ATG TGT GGG 430  
 Gly Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly  
 130 135 140  
 GCC GTC TTC CTC GTG GGA CAA GCC TTC ACG TTC AGA CCC CGC CGC CAT 478  
 Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His  
 145 150 155  
 CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG TAC CCA GGC CAT CTT TCA 526  
 Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser  
 160 165 170 175  
 GGA CAT CGA ATG GCT 541  
 Gly His Arg Met Ala  
 180

## (2) INFORMATION FOR SEQ ID NO: 28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Val Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val  
 1 5 10 15  
 Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly  
 20 25 30  
 Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe Ser Cys Leu Ile His  
 35 40 45  
 Pro Ala Ala Gly Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
 50 55 60  
 Thr Asn Asp Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val  
 65 70 75 80

Ile Leu His Ala Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr  
                             85                            90                            95

Ser Thr Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val  
                             100                            105                            110

Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly  
                             115                            120                            125

Ala Ala Thr Met Cys Ser Ala Leu Tyr Val Gly Asp Met Cys Gly Ala  
                             130                            135                            140

Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg Arg His Gln  
                             145                            150                            155                            160

Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly His Leu Ser Gly  
                             165                            170                            175

His Arg Met Ala  
                             180

## (2) INFORMATION FOR SEQ ID NO: 29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: HCCL153

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..287

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC	47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala	
1                            5                            10                            15	
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG	95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu	
20                            25                            30	
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA	143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
35                            40                            45	
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA	191

Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu  
50 55 60

CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA 239  
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu  
65 70 75

ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA 287  
Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser  
80 85 90 95

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His  
1 5 10 15  
Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr  
20 25 30  
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser  
35 40 45  
Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His  
50 55 60  
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile  
65 70 75 80  
Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser  
85 90 95

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HD10-1-25

09873224.060501  
105090.42267860

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..401

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu	
50 55 60	
GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCG CAA GCC GCC CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA	335
Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA	383
Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu	
115 120 125	
ACC TTC TGG CAC AAG CAT	401
Thr Phe Trp His Lys His	
130	

## (2) INFORMATION FOR SEQ ID NO: 32:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala
1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu  
                   20                                  25                                  30  
 Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys  
                   35                                  40                                  45  
 Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val  
                   50                                  55                                  60  
 Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys  
                   65                                  70                                  75                                  80  
 Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln  
                                   85                                  90                                  95  
 Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln  
                                   100                                  105                                  110  
 Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr  
                                   115                                  120                                  125  
 Phe Trp His Lys His  
                                   130

## (2) INFORMATION FOR SEQ ID NO: 33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: HD10-1-3

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC GTC ACA AAA TAC ATT ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met	
1                                  5                                  10                                  15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTG TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20                                  25                                  30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGC	143



Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly  
                     35                                    40                                    45  
 TGC GTT GTA ATC GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA CTC 191  
 Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu  
                     50                                    55                                    60  
 GTT CCA GAC AAG GAG GTG TTG TAT CAA CAG TAC GAT GAG ATG GAG GAG 239  
 Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu  
                     65                                    70                                    75  
 TGC TCG CAA GCG GCG CCA TAC ATC GAA CAA GCT CAG GTA ATA GCC CAC 287  
 Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His  
                     80                                    85                                    90                                    95  
 CAG TTC AAG GAG AAA ATC CTT GGA CTG CTG CAG CGA GCC ACC CAA CAA 335  
 Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln  
                                     100                                    105                                    110  
 CAA GCT GTC ATT GAG CCC GTA ATA GCT TCC AAC TGG CAA AAG CTT GAA 383  
 Gln Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu  
                                     115                                    120                                    125  
 ACC TTC TGG CAC AAG CAT 401  
 Thr Phe Trp His Lys His  
                     130

## (2) INFORMATION FOR SEQ ID NO: 34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Gln Asn Glu Ile Cys Leu Thr His Pro Val Thr Lys Tyr Ile Met Ala  
   1                                    5                                    10                                    15  
 Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu  
                     20                                    25                                    30  
 Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys  
                     35                                    40                                    45  
 Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Leu Val  
                     50                                    55                                    60  
 Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys  
                     65                                    70                                    75                                    80  
 Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln  
                                     85                                    90                                    95  
 Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln

100

105

110

Ala Val Ile Glu Pro Val Ile Ala Ser Asn Trp Gln Lys Leu Glu Thr  
 115 120 125

Phe Trp His Lys His  
 130

## (2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-164

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..401

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile	
50 55 60	
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GGA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA	335

Gln Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln  
 100 105 110

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG 383  
 Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu  
 115 120 125

GCC TTT TGG CAC AAG CAT 401  
 Ala Phe Trp His Lys His  
 130

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu  
 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys  
 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val  
 50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys  
 65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln  
 85 90 95

Phe Lys Gly Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln  
 100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala  
 115 120 125

Phe Trp His Lys His  
 130

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:  
(B) CLONE: BR36-20-166
- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG	47
Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met	
1 5 10 15	
GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG	95
Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu	
20 25 30	
CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT	143
Leu Gly Gly Val Leu Ala Ala Leu Ala Tyr Cys Leu Ser Val Gly	
35 40 45	
TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC	191
Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile	
50 55 60	
GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG	239
Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu	
65 70 75	
TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTG ATA GCT CAC	287
Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His	
80 85 90 95	
CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA	335
Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln	
100 105 110	
CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG	383
Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu	
115 120 125	
GCC TTT TGG CAC AAG CAT	401
Ala Phe Trp His Lys His	
130	

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 133 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Gln	Asn	Glu	Ile	Cys	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala
1				5					10					15	
Cys	Met	Ser	Ala	Asp	Leu	Glu	Val	Thr	Thr	Ser	Thr	Trp	Val	Leu	Leu
			20					25					30		
Gly	Gly	Val	Leu	Ala	Ala	Leu	Ala	Ala	Tyr	Cys	Leu	Ser	Val	Gly	Cys
		35				40						45			
Val	Val	Ile	Val	Gly	His	Ile	Glu	Leu	Gly	Gly	Lys	Pro	Ala	Ile	Val
	50					55					60				
Pro	Asp	Lys	Glu	Val	Leu	Tyr	Gln	Gln	Tyr	Asp	Glu	Met	Glu	Glu	Cys
	65				70					75					80
Ser	Gln	Ala	Ala	Pro	Tyr	Ile	Glu	Gln	Ala	Gln	Val	Ile	Ala	His	Gln
				85					90					95	
Phe	Lys	Glu	Lys	Val	Leu	Gly	Leu	Leu	Gln	Arg	Ala	Thr	Gln	Gln	Gln
			100					105					110		
Ala	Val	Ile	Glu	Pro	Ile	Val	Thr	Thr	Asn	Trp	Gln	Lys	Leu	Glu	Ala
			115				120					125			
Phe	Trp	His	Lys	His											
	130														

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: BR36-20-165

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 3..401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

TC CAA AAT GAA ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG 47  
 Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met  
 1 5 10 15

GCA TGC ATG TCA GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG 95  
 Ala Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu  
 20 25 30

CTT GGA GGG GTC CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT 143  
 Leu Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly  
 35 40 45

TGT GTT GTG ATT GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC 191  
 Cys Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile  
 50 55 60

GTT CCA GAC AAA GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG 239  
 Val Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu  
 65 70 75

TGC TCA CAA GCT GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC 287  
 Cys Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His  
 80 85 90 95

CAG TTC AAG GAA AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA 335  
 Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln  
 100 105 110

CAA GCT GTC ATT GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG 383  
 Gln Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu  
 115 120 125

GCC TTT TGG CAC AAG CAT 401  
 Ala Phe Trp His Lys His  
 130

## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Gln Asn Glu Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 1 5 10 15

Cys Met Ser Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu  
 20 25 30

Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys  
 35 40 45

Val Val Ile Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val  
50 55 60

Pro Asp Lys Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys  
65 70 75 80

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln  
85 90 95

Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln  
100 105 110

Ala Val Ile Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala  
115 120 125

Phe Trp His Lys His  
130

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 509 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: PC-2-1

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 3..509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
CGC ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	

50	55	60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC			239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro			
65	70	75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG			287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly			
80	85	90	95
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC			335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp			
100	105	110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG			383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr			
115	120	125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC			431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro			
130	135	140	
ATT GGG GGC GTC GCA AGG GGT CTC GCA CAC GGT GTG AGG GTC CTT GAG			479
Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu			
145	150	155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA			509
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu			
160	165		

## (2) INFORMATION FOR SEQ ID NO: 42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn		
1	5	10
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly		
20	25	30
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala		
35	40	45
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro		
50	55	60
Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly		
65	70	75
Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp		



85

90

95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110

Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile  
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160

Gly Val Asn Tyr Ala Thr Gly Asn Leu  
 165

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-2-6

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..509

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
CGC ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	

CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC 239  
 Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro  
 65 70 75  
 GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG 287  
 Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly  
 80 85 90 95  
 TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC 335  
 Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp  
 100 105 110  
 CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG 383  
 Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr  
 115 120 125  
 TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC 431  
 Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro  
 130 135 140  
 ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG 479  
 Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu  
 145 150 155  
 GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA 509  
 Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu  
 160 165

## (2) INFORMATION FOR SEQ ID NO: 44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Val Asn Tyr Ala Thr Gly Asn Leu  
 165

## (2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 580 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-4-1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC	46
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly	
1 5 10 15	
GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC	94
Gly Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val	
20 25 30	
CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT	142
Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser	
35 40 45	
TTC TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC	190
Phe Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala	
50 55 60	
TCT GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT	238

Ser Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn  
 65 70 75  
 GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA 286  
 Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu  
 80 85 90 95  
 CAC GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA 334  
 His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg  
 100 105 110  
 TGC TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GCA GCA 382  
 Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala  
 115 120 125  
 GTC ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT 430  
 Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala  
 130 135 140  
 GCC CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC 478  
 Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe  
 145 150 155  
 TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG 526  
 Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val  
 160 165 170 175  
 CAG AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG 574  
 Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg  
 180 185 190  
 ATG GCA 580  
 Met Ala

## (2) INFORMATION FOR SEQ ID NO: 46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly  
 1 5 10 15  
 Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu  
 20 25 30  
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His  
85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys  
100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val  
115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala  
130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met  
180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: PC-4-6

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..580

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

A ACG TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC  
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly  
1 5 10 15

GGC CCC ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC

46

94

Gly Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val  
20 25 30

CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT 142  
Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser  
35 40 45

TTC TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC  
Phe Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala 190  
50 55 60

TCT GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT  
Ser Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn 238  
65 70 75

GAT TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA  
Asp Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu 286  
80 85 90 95

CAC GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA 334  
His Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg  
100 105 110

TGC TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA 382  
Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala  
115 120 125

GTC ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT 430  
Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala  
130 135 140

GCC CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC  
Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe  
145 150 155

TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG 526  
Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val  
160 165 170 175

CAG AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG 574  
Gln Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg  
180 185 190

ATG GCA  
Met Ala 580

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear -

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly  
 1 5 10 15  
 Pro Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu  
 20 25 30  
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His  
 85 90 95  
 Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val  
 115 120 125  
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175  
 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-3-4

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..959

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CCG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	
130 135 140	
ATT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Ile Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623
Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys	
195 200 205	



CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC GCA 671  
 Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala  
 210 215 220

CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC TGG 719  
 Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp  
 225 230 235

GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC ACG 767  
 Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr  
 240 245 250 255

GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC CTC 813  
 Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu  
 260 265 270

TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG GTA 863  
 Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val  
 275 280 285

GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG AAC 911  
 Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn  
 290 295 300

TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG GCA 959  
 Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO: 50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala  
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60

Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly  
 65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175  
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val  
 180 185 190  
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro  
 195 200 205  
 Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro  
 210 215 220  
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val  
 225 230 235 240  
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala  
 245 250 255  
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys  
 260 265 270  
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly  
 275 280 285  
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys  
 290 295 300  
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 959 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-3-8

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CC ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC	47
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr	
1 5 10 15	
AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT	95
Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val	
20 25 30	
GGC GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC	143
Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg	
35 40 45	
GCG ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG	191
Ala Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln	
50 55 60	
CCT ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC	239
Pro Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro	
65 70 75	
GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG	287
Gly Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly	
80 85 90 95	
TGG CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC	335
Trp Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp	
100 105 110	
CCC CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG	383
Pro Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr	
115 120 125	
TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	431
Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro	
130 135 140	
GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG	479
Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu	
145 150 155	
GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC TCT	527
Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
160 165 170 175	
ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT GCA	575
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
180 185 190	
GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT TGC	623

Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys		
			195					200					205				
CCA	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCA	GAT	AAC	CTG	ATC	CTA	CAC	GCA		671
Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala		
		210					215					220					
CCT	GGT	TGC	GTG	CCT	TGT	GTC	ATG	ACA	GGT	AAT	GTG	AGT	AGA	TGC	TGG		719
Pro	Gly	Cys	Val	Pro	Cys	Val	Met	Thr	Gly	Asn	Val	Ser	Arg	Cys	Trp		
	225					230					235						
GTC	CAA	ATT	ACC	CCT	ACA	CTG	TCA	GCC	CCG	AGC	CTC	GGA	GCA	GTC	ACG		767
Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Ser	Leu	Gly	Ala	Val	Thr		
240					245					250					255		
GCT	CCT	CTT	CGG	AGA	GCC	GTT	GAC	TAC	CTA	GCG	GGA	GGG	GCT	GCC	CTC		815
Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	Gly	Gly	Ala	Ala	Leu		
			260					265					270				
TGC	TCC	GCG	TTA	TAC	GTA	GGA	GAC	GCG	TGT	GGG	GCA	CTA	TTC	TTG	GTA		863
Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	Gly	Ala	Leu	Phe	Leu	Val		
		275						280					285				
GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	CGC	CAG	CAC	GCT	ACG	GTG	CAG	AAC		911
Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	Gln	His	Ala	Thr	Val	Gln	Asn		
	290						295					300					
TGC	AAC	TGT	TCC	ATT	TAC	AGT	GGC	CAT	GTT	ACC	GGC	CAC	CGG	ATG	GCA		959
Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	His	Val	Thr	Gly	His	Arg	Met	Ala		
	305					310					315						

## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn		
1				5					10					15			
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly		
		20						25					30				
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Met	Gly	Val	Arg	Ala		
		35					40					45					
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro		
		50				55					60						
Ile	Pro	Lys	Ala	Arg	Gln	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly		
		65			70					75					80		

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
                                     85                                    90                                    95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
                                     100                                    105                                    110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
                                     115                                    120                                    125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val  
                                     130                                    135                                    140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
                                     145                                    150                                    155                                    160  
 Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
                                     165                                    170                                    175  
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val  
                                     180                                    185                                    190  
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro  
                                     195                                    200                                    205  
 Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro  
                                     210                                    215                                    220  
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val  
                                     225                                    230                                    235                                    240  
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala  
                                     245                                    250                                    255  
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys  
                                     260                                    265                                    270  
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly  
                                     275                                    280                                    285  
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys  
                                     290                                    295                                    300  
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala  
                                     305                                    310                                    315

## (2) INFORMATION FOR SEQ ID NO: 53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 959 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC C/E1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CCATGAGCAC GAATCCTAAA CCTCAAAGAA AAACCAAAG AAACACCAAC CGTCGCCAC	60
AGGACGTCAA GTTCCCGGGC GGTGGTCAGA TCGTTGGCGG AGTTTACTTG TTGCCGCGCA	120
GGGGCCCTAG GATGGGTGTG CCGCGACTC GGAAGACTTC GGAACGGTCG CAACCCCGTG	180
GACGGCGTCA GCCTATTCCC AAGGCGCGCC AGCCACGGG CCGGTCCTGG GGTCAACCCG	240
GGTACCCTTG GCGCCCTTAC GCCAATGAGG GCCTCGGGTG GGCAGGGTGG CTGCTCTCCC	300
CTCGAGGCTC TCGGCCTAAT TGGGGCCCA ATGACCCCG GCGAAAATCG CGTAATTTGG	360
GTAAGGTCAT CGATACCCTA ACCTGCGGAT TCGCCGATCT CATGGGGTAY ATCCCGCTCG	420
TAGGCGGCCC CRTTGGGGGC GTCCCAAGGG CTCTCGCACA CGGTGTGAGG GTCCTTGAGG	480
ACGGGGTAAA CTATSCAACA GCGAATTAC CCGGTTGCTC TTTCTCTATC TTTATTCTTG	540
CTCTCTCTC GTGTCTGACC GTTCCGGCCT CTGCAGTTCC CTACCGAAAT GCCTCTGGGA	600
TTTATCATGT TACCAATGAT TGCCCAAAC CTTCATAGT CTATGAGGCA GATAACCTGA	660
TCCTACACGC ACCTGGTTGC GTGCCTTGTG TCATGACAGG TAATGTGAGT AGATGCTGGG	720
TCCAAATTAC CCCTACACTG TCAGCCCGCA GCCTCGGAGC AGTCACGGCT CCTCTTCGGA	780
GAGCCGTTGA CTACCTAGCG GGAGGGGCTG CCCTCTGCTC CGCGTTATAC GTAGGAGACG	840
CGTGTGGGGC ACTATTCTTG GTAGGCCAAA TGTTCACTA TAGGCCTCGC CAGCACGCTA	900
CGGTGCAGAA CTGCAACTGT TCCATTTACA GTGGCCATGT TACCGGCCAC CGGATGGCA	959

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1					5				10					15	

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Val  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175  
 Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Val  
 180 185 190  
 Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp Cys Pro  
 195 200 205  
 Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His Ala Pro  
 210 215 220  
 Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys Trp Val  
 225 230 235 240  
 Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val Thr Ala  
 245 250 255  
 Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala Leu Cys  
 260 265 270  
 Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu Val Gly  
 275 280 285  
 Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln Asn Cys  
 290 295 300  
 Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met Ala  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 354 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: PC-1-37

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..354

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

```

ACCACCGGAG CTTCTATCAG ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT      60
TCAGGCGGGG CGCATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCACC      120
ATTCTTGGGA TAGGCACTGT CCTTGACCAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC      180
TTGGCCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCC ACCCCAACAT CGAGGAAGTG      240
GCCCTGCCTC AGGAGGGGGA GGTTCCTTC TACGGCAGAG CCATTCCCCT TGCTTTTATA      300
AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA ATTGTGATGA ACTC          354
  
```

## (2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 118 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

```

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
 1              5              10              15

Asp Gly Gly Cys Ser Gly Gly Ala His Asp Val Ile Ile Cys Asp Glu
      20              25              30
  
```



Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu  
 35 40 45  
 Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Xaa  
 50 55 60  
 Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val  
 65 70 75 80  
 Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala Ile Pro  
 85 90 95  
 Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys  
 100 105 110  
 Lys Asn Cys Asp Glu Leu  
 115

## (2) INFORMATION FOR SEQ ID NO: 57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-43

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..354

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

ACCACCGGAG CTTCTATCAC ATACTCCACT TACGGCAAGT TCCTTGCTGA TGGAGGGTGT 60  
 TCAGGCGGCG CGTATGACGT GATCATATGC GACGAGTGCC ATTCCCAGGA CGCCACCACC 120  
 ATTCTTGGGA TAGGCACTGT CCTTGACCAG GCAGAGACGG CTGGAGCTAG GCTCGTCGTC 180  
 TTGGNCACGG NCACCCCTCC CGGCAGTGTG ACAACGCCCC ACCCCAACAT CGAGGARGTG 240  
 GCCCTGCCTC AGGAGGGGGA GGTTCCTTC TACGGNAGAG CCATTCCCTC TGCTTTTATA 300  
 AAGGGTGGTA GGCATCTCAT CTTCTGCCAT TCCAAGAAAA AATGTGATGA ACTT 354

## (2) INFORMATION FOR SEQ ID NO: 58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```

Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala
1          5          10          15
Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys Asp Glu
          20          25          30
Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr Val Leu
          35          40          45
Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Xaa Thr Xaa
          50          55          60
Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu Glu Val
          65          70          75          80
Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Xaa Arg Ala Ile Pro
          85          90          95
Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His Ser Lys
          100          105          110
Lys Lys Cys Asp Glu Leu Arg Gln Ala Thr Asp Gln Pro Gly Arg Glu
          115          120          125
Arg Pro Trp Glu Tyr
          130

```

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 357 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-37

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ATGGCTTTCA TGTCTCCGGA CTTGGAGGTC ATTACCANCA CTTGGGTTCT GGTGGGGGGC      60
GTTGTGGGCA CCCTGNCNC CTACTGTTG ACGGTGGGTT CCGTAGCCAT AGTCGGTAGG      120
ATCATCCTCT CTGGGAAACC TGCCATCATT NCCGATAGGG AGGTATTATA CCAGCAATTT      180
GATGAGATGG AGGAGTGCTC GGCCTCGTTG CCCTATATGG ACGAAACACG TNCATTGCC      240
GGACAATTCA AAGAGAAAGT GCTCGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT      300
CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGATC AGTTCTGGNC CACATAC      357

```

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

```

Met Ala Phe Met Ser Pro Asp Leu Glu Val Ile Thr Xaa Thr Trp Val
1           5           10           15
Leu Val Gly Gly Val Val Ala Thr Leu Xaa Xaa Tyr Cys Leu Thr Val
20           25           30
Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala
35           40           45
Ile Ile Xaa Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu
50           55           60
Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Xaa Ile Ala
65           70           75           80
Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln
85           90           95
Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala
100          105          110
Asp Gln Phe Trp Xaa Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln
115          120          125

```

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: PC-1-48

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

```

ATGGCCTTGCA TGTCTGCGGA CCTGGAGGTC ATTACCANCA CTTGGGTTCT GGTGGGGGGC      60
GTTGTGGCGN CCTGGCGGCT CTACTGCTTG ACGGTGGGTT CGGTAGCCAT AGTCGGTAGG      120
ATCATCCTCT CTGGGAAACC TGCCATCATT CCCGATAGGG AGGCATTATA CCANCAATTT      180
GATGAGATGG AGGAGTGCTC GGCCTCGTTG CCTATATGG ACGAGACACG TGCCATTGCC      240
GCACAATTCA AAGAGAAAGT GCTCGGCTTC ATCAGCACGA CCGGCCAGAA GGCTGAAACT      300
CTGAAGCCGG CAGCCACGTC TGTGTGGAAC AAGGCTGANC AGTTCTGGGC CACATAC      357

```

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

```

Met Ala Cys Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val
1              5              10              15

Leu Val Gly Gly Val Val Ala Xaa Leu Ala Ala Tyr Cys Leu Thr Val
                20              25              30

Gly Ser Val Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala
35              40              45

Ile Ile Pro Asp Arg Glu Ala Leu Tyr Xaa Gln Phe Asp Glu Met Glu
50              55              60

```

Glu Cys Ser Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala  
 65 70 75 80

Gly Gln Phe Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln  
 85 90 95

Lys Ala Glu Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala  
 100 105 110

Xaa Gln Phe Trp Ala Thr Tyr Met Trp Asn Phe Ile Ser Gly Ile Gln  
 115 120 125

## (2) INFORMATION FOR SEQ ID NO: 63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP-161"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

ACCGGAGGCC AGGAGAGTGA TCTCCTCC

28

## (2) INFORMATION FOR SEQ ID NO: 64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iii) ANTI-SENSE: YES

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP-162"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GGGCTGCTCT ATCCTCATCG ACGCCATC

28

(2) INFORMATION FOR SEQ ID NO: 65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl63"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GCCAGAGGCT CGGAAGGCGA TCAGCGCT

28

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl64"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GAGCTGCTCT GTCCTCCTCG ACGCCGCA

28

(2) INFORMATION FOR SEQ ID NO: 67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPPr23"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

CTCATGGGGT ACATTCCGCT

20

## (2) INFORMATION FOR SEQ ID NO: 68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPPr54"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

CTATTACCAG TTCATCATCA TATCCCA

27

## (2) INFORMATION FOR SEQ ID NO: 69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPri116"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

TTTTAAATAC ATCATGRCTG YATG

24

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPri66"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CTATTATTGT ATCCCRCTGA TGAARTTCCA CAT

33

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc\_feature



- (B) LOCATION: 1..28  
(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl18:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ACTAGTCGAC TAYTGATCCR CTATRWARTT CCACAT

36

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..28  
(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl17:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

TTTTAAATAC ATCGCRCTGC ATGCA

25

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1..28  
(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl19:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

ACTAGTCGAC TARTTGCATA GCCKRTTCAT CCAYTG

36

## (2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl31:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GGAATTCTAG ACCTCTGGGA YGARAYTGGA ARTG

34

## (2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl30:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

GGAATTCTAG ACGCTAYCAR GCACGTTGYG C

31

## (2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl34:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CATATAGATG CCCACTTCCT ATC

23

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCPrl3:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTGTGCCAGG ACCATC

16

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP:r4:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

GACATGCATG TCATGATGTA

20

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1..28

(D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP:r152:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TACGCCTCTT CTATATCGGT TGGGGCCTG

29

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP152:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ATGTTGGGTA AGGTCATCGA TACCCT

25

## (2) INFORMATION FOR SEQ ID NO: 81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP141:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCCCGGGAGGT CTCGTAGACC GTGCA

25

## (2) INFORMATION FOR SEQ ID NO: 82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iii) ANTI-SENSE: YES

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..28
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer  
HCP140:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CTATTAAAGA TAGAGAAAGA GCAACCGGG

29

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 192 to 203 of the V1 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 223 of the V2 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	His	Thr
1				5				10		

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 213 to 233 of the V2 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	His	Ala
1				5				10		

(2) INFORMATION FOR SEQ ID NO: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Val Gln Asp Gly Asn Thr Ser Thr Cys Trp Thr Pro Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 242 of the V3 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Val Met Thr Gly Asn Val Ser Arg Cys Trp Val Gln Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

Val Arg Tyr Val Gly Ala Thr Thr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ala	Pro	Ser	Leu	Gly	Ala	Val	Thr	Ala	Pro
1				5					10

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

Arg	Pro	Arg	Arg	His	Gln	Thr	Val	Gln	Thr
1				5					10

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 294 to 303 of the V5 region of HCV  
type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Arg Pro Arg Gln His Ala Thr Val Gln Asn  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 70 to 78 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

Gln Pro Thr Gly Arg Ser Trp Gly Gln  
 1 5

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR33 and BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV  
 type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Val Gln Asp Gly Asn Thr Ser Thr  
 1 5

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 230 to 237 of the V3 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

Val Gln Asp Gly Asn Thr Ser Ala  
1 5

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN PROTEIN:

(B) MAP POSITION: positions 248 to 257 of the V4 region of HCV  
type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

## (viii) POSITION IN GENOME:

(B) MAP POSITION: Positions 1688 to 1707 of HCV type 3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

Leu	Gly	Gly	Lys	Pro	Ala	Ile	Val	Pro	Asp	Lys	Glu	Val	Leu	Tyr	Gln
1				5				10					15		
Gln Tyr Asp Glu															
20															

## (2) INFORMATION FOR SEQ ID NO: 98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

## (viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 3

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

Leu	Gly	Gly	Lys	Pro	Ala	Leu	Val	Pro	Asp	Lys	Glu	Val	Leu	Tyr	Gln
1				5				10					15		
Gln Tyr Asp Glu															
20															

## (2) INFORMATION FOR SEQ ID NO: 99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

## (viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1712 to 1731

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

Ser Gln Ala Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln  
1 5 10 15

Phe Lys Glu Lys  
20

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: BR36

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

Ile Ala His Gln Phe Lys Glu Lys Val Leu Gly Leu Leu Gln Arg Ala  
1 5 10 15

Thr Gln Gln Gln  
20

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: HD10

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

Ile Ala His Gln Phe Lys Glu Lys Ile Leu Gly Leu Leu Gln Arg Ala  
1 5 10 15

Thr Gln Gln Gln  
20

(2) INFORMATION FOR SEQ ID NO: 102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Ala Leu Tyr Gln  
1 5 10 15

Gln Phe Asp Glu  
20

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1688 to 1707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val Leu Tyr Gln  
1 5 10 15

Gln Phe Asp Glu  
20

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: position 1712 to 1731 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Ser	Ala	Ser	Leu	Pro	Tyr	Met	Asp	Glu	Thr	Arg	Ala	Ile	Ala	Gly	Gln
1				5					10					15	
Phe	Lys	Glu	Lys												
				20											

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(viii) POSITION IN GENOME:

(B) MAP POSITION: positions 1724 to 1743 of HCV type 5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

Ile	Ala	Gly	Gln	Phe	Lys	Glu	Lys	Val	Leu	Gly	Phe	Ile	Ser	Thr	Thr
1					5				10					15	
Gly	Gln	Lys	Ala												
				20											

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB48-3-10

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTC TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GCA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGT CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AAA	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys	
65 70 75	
GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG	286
Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC GCT GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA CCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu	
100 105 110	
GGA GCC	340
Gly Ala	

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15



Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
 50 55 60  
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Lys Ala  
 65 70 75 80  
 Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Pro Leu Gly  
 100 105 110  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: GB116-3-5

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTA TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AGA GCA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAC GTG GGC GGT CCC ATG CAT AAC AGC AGG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp	
35 40 45	

CTG TGC GGG TAT CGC AGA TGC CGT GCG AGC GGC GTC TAC ACC ACC AGC 190  
 Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser  
           50                          55                          60

TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCT ATC AGA 238  
 Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg  
           65                          70                          75

GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG 286  
 Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu  
           80                          85                          90                          95

GTC GTC ATT GCT GAA AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC 334  
 Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu  
                           100                          105                          110

GGA GCC 340  
 Gly Ala

## (2) INFORMATION FOR SEQ ID NO: 109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln  
   1                          5                          10                          15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Thr Ala Leu Thr  
                           20                          25                          30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu  
                           35                          40                          45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
           50                          55                          60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala  
   65                          70                          75                          80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                           85                          90                          95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly  
                           100                          105                          110

Ala

## (2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB215-3-8

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

C TCC ACT GTA ACC GAA AAA GAC ATC AGG GTC GAG GAG GAG GTA TAT	46
Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCC GAA GCC CGC AAG GTA ATT ACC GCC CTA	94
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu	
20 25 30	
ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAT AGC AAA GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp	
35 40 45	
CTG TGC GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACA CTG ACG TGC TAT CTC AAA GCC TCA GCC GCC ATC AGG	238
Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg	
65 70 75	
GCG TCA GGG CTG AGA GAC TGC ACT ATG CTG GTC TAT GGT GAC GAC CTG	286
Ala Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATT GCC GAG AGC GAT GGC GTA GAG GAG GAC AAA CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu	
100 105 110	
GGA GTC	340
Gly Val	

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
 1             5             10             15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
          20             25             30
Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
          35             40             45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
          50             55             60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
          65             70             75             80
Ser Gly Leu Arg Asp Cys Thr Met Leu Val Tyr Gly Asp Asp Leu Val
          85             90             95
Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly
          100            105            110
Val

```

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB358-3-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

C TCC ACT GTA ACC GAA AAG GAC ATC AGG GTC GAG GAG GAG GTG TAT

46

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr  
 1 5 10 15

CAG TGT TGT GAC CTG GAG CCC GAG GCC CGC AAG GCA ATT ACT GCC CTA 94  
 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu  
 20 25 30

ACA GAG AGA CTC TAT GTG GGC GGT CCC ATG CAT AAC AGC AAG GGA GAC 142  
 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp  
 35 40 45

CTG TGT GGG TAT CGC AGA TGC CGC GCA AGC GGC GTC TAC ACC ACC AGC 190  
 Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser  
 50 55 60

TTC GGG AAC ACA CTG ACG TGC TAC CTC AAA GCC TCA GCC GCT ATC AGA 238  
 Phe Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg  
 65 70 75

GCG GCG GGG CTG AGA GAC TGC ACC ATG TTG GTC TGT GGT GAT GAC CTG 286  
 Ala Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu  
 80 85 90 95

GTC GTC ATC GCT GAG AGC GAT GGC GTT GAG GAG GAC AAA CGA GCC CTC 334  
 Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu  
 100 105 110

GGA GCC 340  
 Gly Ala

## (2) INFORMATION FOR SEQ ID NO: 113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Val Tyr Gln  
 1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Thr Ala Leu Thr  
 20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu  
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala  
 65 70 75 80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Lys Arg Ala Leu Gly  
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: G3549-3-6

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

C	TCC	ACG	GTG	ACC	GAA	AGG	GAT	ATC	AGG	ACC	GAG	GAA	GAG	ATC	TAC	46
	Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Glu	Ile	Tyr	
	1				5					10					15	
CAG	TGC	TGC	GAC	CTG	GAG	CCC	GAA	GCC	CGC	AAG	GTG	ATA	TCC	GCC	CTA	94
Gln	Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Ser	Ala	Leu	
				20					25					30		
ACG	GAA	AGA	CTC	TAC	GTG	GGC	GGT	CCC	ATG	TAC	AAC	TCC	AAG	GGG	GAC	142
Thr	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Tyr	Asn	Ser	Lys	Gly	Asp	
			35					40					45			
CTA	TGC	GGG	CAA	CGG	AGG	TGC	CGC	GCA	AGC	GGG	GTC	TAC	ACC	ACC	AGC	190
Leu	Cys	Gly	Gln	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr	Ser	
		50					55					60				
TTC	GGG	AAC	ACT	GTA	ACG	TGT	TAT	CTC	AAG	GCC	GTT	GCG	GCT	ACT	AGG	238
Phe	Gly	Asn	Thr	Val	Thr	Cys	Tyr	Leu	Lys	Ala	Val	Ala	Ala	Thr	Arg	
	65					70					75					
GCC	GCA	GGT	CTG	AAA	GGT	TGC	AGC	ATG	CTG	GTT	TGT	GGA	GAC	GAC	TTA	286
Ala	Ala	Gly	Leu	Lys	Gly	Cys	Ser	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	
	80				85					90					95	

GTC	GTC	ATC	TGC	GAG	AGC	GGC	GGC	GTA	GAG	GAG	GAT	GCA	AGA	GCC	CTC	334
Val	Val	Ile	Cys	Glu	Ser	Gly	Gly	Val	Glu	Glu	Asp	Ala	Arg	Ala	Leu	
				100					105					110		
CGA	GCC															340
Arg	Ala															

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln
  1              5              10              15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr
      20              25              30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
      35              40              45

Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
      50              55              60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala
      65              70              75              80

Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val
      85              90              95

Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
      100             105             110

Ala

```

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: GB809-3-1

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

C TCC ACT GTG ACT GAG AGA GAC ATC AAG GTC GAA GAA GAA GTC TAT 46  
 Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr  
 1 5 10 15  
 CAG TGT TGT GAT CTG GAG CCC GAG GCC CGC AAG GTA ATA GCC GCC CTC 94  
 Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu  
 20 25 30  
 ACG GAG AGA CTC TAC GTG GGC GGC CCC ATG CAT AAC AGC AAG GGA GAC 142  
 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp  
 35 40 45  
 CTT TGC GGG TAT CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACC AGC 190  
 Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser  
 50 55 60  
 TTC GGG AAC ACA ATG ACG TGC TAC CTT AAG GCC TCA GCA GCC ATC AGG 238  
 Phe Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg  
 65 70 75  
 GCT GCG GGG CTA AAG GAT TGC ACC ATG CTG GTT TGC GGT GAC GAC CTA 286  
 Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu  
 80 85 90 95  
 GTC GTG ATC GCC GAG AGC GGT GGC GTT GAG GAG GAC AAA CGA GCC CTC 334  
 Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu  
 100 105 110  
 GGA GCT  
 Gly Ala 340

## (2) INFORMATION FOR SEQ ID NO: 117:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ser Thr Val Thr Glu Arg Asp Ile Lys Val Glu Glu Glu Val Tyr Gln  
 1 5 10 15



Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ala Ala Leu Thr  
                   20                                  25                                  30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu  
                   35                                  40                                  45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
                   50                                  55                                  60  
 Gly Asn Thr Met Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala  
                   65                                  70                                  75                                  80  
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                                   85                                  90                                  95  
 Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly  
                   100                                  105                                  110  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 118:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: GB358-4-1

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1                                  5                                  10                                  15	
CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20                                  25                                  30	
GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35                                  40                                  45	

TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG 192  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
 50 55 60

GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC 240  
 Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80

TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC 288  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His  
 85 90 95

CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC 336  
 Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
 100 105 110

TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG 384  
 Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
 115 120 125

CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT 432  
 Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140

GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTC TTG 480  
 Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160

GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG 528  
 Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG A 574  
 Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg  
 180 185 190

## (2) INFORMATION FOR SEQ ID NO: 119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser

50

55

60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His  
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr  
130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg  
180 185 190

## (2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 574 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: GB549-4-3

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC 48  
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15

CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG 96  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30

GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT 144  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
           35                  40                  45  
 TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG 192  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
           50                  55                  60  
 GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC 240  
 Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp  
           65                  70                  75                  80  
 TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT 288  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
                   85                  90                  95  
 CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC 336  
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys  
                   100                  105                  110  
 TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG 384  
 Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro  
           115                  120                  125  
 CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC 432  
 Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
           130                  135                  140  
 GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG 480  
 Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
           145                  150                  155                  160  
 GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CGC CAT TGG ACT ACC CAG 528  
 Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
                   165                  170                  175  
 GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA A 574  
 Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg  
           180                  185                  190

## (2) INFORMATION FOR SEQ ID NO: 121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
   1                  5                  10                  15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
           20                  25                  30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys  
 100 105 110  
 Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro  
 115 120 125  
 Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg  
 180 185 190

## (2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 574 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GB809-4-3

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC

48

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	
1				5					10					15		
CCC	GTT	GGG	GGC	GTC	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	AGG	GCT	GTG	96
Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val	
			20					25					30			
GAG	GAC	GGG	ATT	AAC	TAT	GCG	ACA	GGG	AAT	CTT	CCC	GGT	TGC	TCT	TTC	144
Glu	Asp	Phe	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	
		35				40					45					
TCT	ATC	TTC	CTC	CTG	GCA	CTT	CTT	TCG	TGC	CTC	ACT	GTC	CCA	GCG	TCA	192
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	
		50				55					60					
GCT	GAG	CAC	TAC	CGG	AAT	GCT	TCG	GGC	ATC	TAT	CAC	ATC	ACC	AAT	GAC	240
Ala	Glu	His	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp	
		65			70				75					80		
TGT	CCG	AAT	TCC	AGC	GTA	GTC	TAT	GAA	ACT	GAC	CAC	CAT	ATA	TTG	CAC	288
Cys	Pro	Asn	Ser	Ser	Val	Val	Tyr	Glu	Thr	Asp	His	His	Ile	Leu	His	
				85					90					95		
TTG	CCG	GGG	TGC	GTA	CCC	TGC	GTG	AGG	GCC	GGG	AAC	GTG	TCT	CGT	TGC	336
Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Ala	Gly	Asn	Val	Ser	Arg	Cys	
			100					105					110			
TGG	ACG	CCG	GTA	ACA	CCT	ACG	GTG	GCT	GCC	GTA	TCC	ATG	GAC	GCT	CCG	384
Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Ala	Val	Ser	Met	Asp	Ala	Pro	
		115				120						125				
CTC	GAG	TCC	TTC	CGG	CGG	CAT	GTG	GAC	CTA	ATG	GTA	GGT	GCG	GCC	ACC	432
Leu	Glu	Ser	Phe	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr	
		130				135					140					
GTG	TGT	TCT	GTC	CTC	TAT	GTT	GGA	GAC	CTC	TGT	GGA	GGT	GCT	TTC	CTA	480
Val	Cys	Ser	Val	Leu	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Gly	Ala	Phe	Leu	
	145				150					155					160	
GTG	GGG	CAG	ATG	TTC	ACC	TTC	CAG	CCG	CGT	CGC	CAC	TGG	ACC	ACG	CAG	528
Val	Gly	Gln	Met	Phe	Thr	Phe	Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	
			165						170				175			
GAT	TGT	AAT	TGC	TCC	ATC	TAT	ACT	GGC	CAT	ATC	ACC	GGC	CAC	AGG	A	574
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly	His	Ile	Thr	Gly	His	Arg		
		180						185				190				

## (2) INFORMATION FOR SEQ ID NO: 123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro  
 115 120 125  
 Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg  
 180 185 190

## (2) INFORMATION FOR SEQ ID NO: 124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..31
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer HCP206"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TGGGGATCCC GTATGATACC CGCTGCTTTG A

31

## (2) INFORMATION FOR SEQ ID NO: 125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: /standard\_name= "HCV Primer HcPr207"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GGCGGAATTC CTGGTCATAG CCTCCGTGAA

30

## (2) INFORMATION FOR SEQ ID NO: 126:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val	Asn	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile
1				5					10		

## (2) INFORMATION FOR SEQ ID NO: 127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Amino acid

(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Amino acid

(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val Tyr Glu Thr Glu His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Val Tyr Glu Ala Asp His His Ile Met His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Val Tyr Glu Thr Asp His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Val Arg Val Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Val Arg Thr Gly Asn Thr Ser Arg Cys Trp Val Pro Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid
- (C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Val Arg Ala Gly Asn Val Ser Arg Cys Trp Thr Pro Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ala	Pro	Tyr	Ile	Gly	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala	Pro	Tyr	Val	Gly	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: amino acid

(C) INDIVIDUAL ISOLATE: GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Ala	Val	Ser	Met	Asp	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: GB358 and GB809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: amino acid  
(C) INDIVIDUAL ISOLATE: GB549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Arg Pro Arg Arg His Trp Thr Thr Gln Asp  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGGGATATGA TGATGAACTG GTC

23

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

CCAGGTACAA CCGAACCAAT TGCC

24

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 957 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..957

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACT AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT	96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTA TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACG AGG AAA ACT TCC GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAA GAT CGG CGC CCC ACT GGC AAG TCC TGG GGA AAA CCA GGA	240
Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly	
65 70 75 80	
TAC CCT TGG CCC CTG TAC GGG AAT GAG GGC CTC GGC TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCC CCC CGA GGG TCT CGC CCG TCA TGG GGC CCA ACT GAC CCC	336
Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro	
100 105 110	
CGG CAC AGG TCA CGC AAC TTG GGT AAG GTC ATC GAT ACC CTT ACG TGT	384
Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys	
115 120 125	
GGC TTT GCC GAC CTC ATG GGG TAC ATC CCT GTC GTC GGC GCC CCA GTT	432
Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val	
130 135 140	
GGT GGT GTC GCC AGA GCT CTC GCG CAT GGC GTG AGA GTT CTG GAA GAC	480
Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp	
145 150 155 160	

GGG ATA AAC TAT GCA ACA GGG AAC TTG CCC GGT TGC TCC TTT TCT ATC 528  
 Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175

TTC TTA TTG GCC CTG CTA TCT TGT ATC ACT GTG CCG GTC TCC GGC TTG 576  
 Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu  
 180 185 190

CAG GTC AAG AAC ACC AGC AGC TCT TAC ATG GTA ACC AAT GAC TGC CAG 624  
 Gln Val Lys Asn Thr Ser Ser Tyr Met Val Thr Asn Asp Cys Gln  
 195 200 205

AAC AGT AGC ATC GTC TGG CAG CTC AGG GAT GCT GTT CTT CAC GTC CCC 672  
 Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro  
 210 215 220

GGG TGT GTC CCT TGT GAG GAG AAG GGC AAC ATA TCC CGC TGT TGG ATA 720  
 Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile  
 225 230 235 240

CCG GTT TCG CCC AAT ATA GCT GTG AGC CAA CCT GGT GCG CTT ACC AAG 768  
 Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys  
 245 250 255

GGC CTG CGG ACG CAT ATT GAT ACC ATC ATT GCA TCC GCT ACG TTT TGC 816  
 Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys  
 260 265 270

TCT GCC CTG TAC ATA GGA GAC CTG TGT GGC GCG GTG ATG TTG GCT TCT 864  
 Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser  
 275 280 285

CAA GTC TTC ATC ATC TCG CCC CAG CAT CAT AAG TTT GTC CAG GAC TGC 912  
 Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys  
 290 295 300

AAC TGT TCC ATA TAC CCA GGC CAC ATC ACT GGA CAT CGG ATG GCG 957  
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala  
 305 310 315

## (2) INFORMATION FOR SEQ ID NO: 144:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30



Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Asp Arg Arg Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
 100 105 110  
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val Gly Ala Pro Val  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile  
 165 170 175  
 Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Gly Leu  
 180 185 190  
 Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val Thr Asn Asp Cys Gln  
 195 200 205  
 Asn Ser Ser Ile Val Trp Gln Leu Arg Asp Ala Val Leu His Val Pro  
 210 215 220  
 Gly Cys Val Pro Cys Glu Glu Lys Gly Asn Ile Ser Arg Cys Trp Ile  
 225 230 235 240  
 Pro Val Ser Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Leu Thr Lys  
 245 250 255  
 Gly Leu Arg Thr His Ile Asp Thr Ile Ile Ala Ser Ala Thr Phe Cys  
 260 265 270  
 Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Ala Val Met Leu Ala Ser  
 275 280 285  
 Gln Val Phe Ile Ile Ser Pro Gln His His Lys Phe Val Gln Asp Cys  
 290 295 300  
 Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met Ala  
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 2..337

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

C TCA ACG GTC ACG GAG AGG GAC ATC AGA ACT GAG GAG TCC ATA TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CTT GCT TGC TCT TTA CCC GAG CAG GCA CGG ACT GCC ATA CAC TCA CTG	94
Leu Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu	
20 25 30	
ACT GAG AGG CTT TAC GTG GGA GGG CCC ATG CTA AAC AGC AAA GGG CAA	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln	
35 40 45	
ACC TGC GGA TAC AGA CGC TGC CGC GCC AGC GGA GTG TTC ACC ACT AGC	190
Thr Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGA AAT ACC ATC ACG TGC TAC GTG AAG GCA CAA GCA GCC TGT AAG	238
Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys	
65 70 75	
GCT GCG GGC ATA ATT GCC CCC ACG ATG CTG GTG TGC GGC GAC GAT CTA	286
Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTT GTC ATC TCA GAG AGT CAG GGG ACC GAG GAG GAC GAG CGG AAC CTA	334
Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu	
100 105 110	
CGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
 1              5              10              15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
          20              25              30
Glu Arg Leu Tyr Val Gly Gly Pro Met Leu Asn Ser Lys Gly Gln Thr
          35              40              45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met
          50              55              60
Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Gln Ala Ala Cys Lys Ala
          65              70              75              80
Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
          85              90              95
Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
          100              105              110

```

Ala

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 345 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..345

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

ATG AGC ACA CTT CCT AAA CCA CAA AGA AAA ACC AAA AGA AAC ACC AAC

48

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15

CCC GGC CAC AGG ACG TTA AGT TCC CAG GCG GCG GTC AGA TCG TTG GTG 96  
 Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val  
 20 25 30

GAG TTT ACG TGC TAC CAC GCA GGG GCC CCC AGT TGG GTG TGC GTG CAG 144  
 Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln  
 35 40 45

TGC GCA AGA CTT CCG AGC GGT CGC AAC CTC GCA GTA GGC GCC AAC CCA 192  
 Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro  
 50 55 60

TCC CCA GGG CGC GCC GAA CCG AGG GCA GGT CCT GGG CTC AGC CCG GGT 240  
 Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly  
 65 70 75 80

ACC CTT GGC CCC TAT ATG GGA ATG AGG GCT GCG GGT GGG CAG GGT GGC 288  
 Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly  
 85 90 95

TCC TGT CCC CGC GCG GCT CTC GCC CGT CGT GGG GCC CAA ATG ACC CCC 336  
 Ser Cys Pro Arg Ala Ala Leu Ala Arg Gly Ala Gln Met Thr Pro  
 100 105 110

GGC GCA GGA 345  
 Gly Ala Gly  
 115

## (2) INFORMATION FOR SEQ ID NO: 148:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15

Pro Gly His Arg Thr Leu Ser Ser Gln Ala Ala Val Arg Ser Leu Val  
 20 25 30

Glu Phe Thr Cys Tyr His Ala Gly Ala Pro Ser Trp Val Cys Val Gln  
 35 40 45

Cys Ala Arg Leu Pro Ser Gly Arg Asn Leu Ala Val Gly Ala Asn Pro  
 50 55 60

Ser Pro Gly Arg Ala Glu Pro Arg Ala Gly Pro Gly Leu Ser Pro Gly  
 65 70 75 80

Thr Leu Gly Pro Tyr Met Gly Met Arg Ala Ala Gly Gly Gln Gly Gly

85

90

95

Ser Cys Pro Arg Ala Ala Leu Ala Arg Arg Gly Ala Gln Met Thr Pro  
 100 105 110

Gly Ala Gly  
 115

## (2) INFORMATION FOR SEQ ID NO: 149:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..280

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..277

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

G GCC TGT GAC CTC AAG GAC GAG GCT AGG AGG GTG ATA ACT TCA CTC	46
Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu	
1 5 10 15	
ACG GAG CGG CTT TAC TGT GGT GGT CCT ATG TTC AAC AGC AAG GGA CAA	94
Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln	
20 25 30	
CAC TGC GGT TAC CGC CGC TGC CGT GCT AGT GGG GTG CTA CCC ACC AGC	142
His Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser	
35 40 45	
TTC GGG AAC ACA ATC ACC TGT TAC ATC AAA GCA AAG GCA GCT ACC AAA	190
Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys	
50 55 60	
GCT GCC GGA ATT AAA AAT CCA TCA TTC CTT GTC TGC GGA GAT GAC TTG	238
Ala Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu	
65 70 75	
GTC GTG ATT GCT GAG AGT GCA GGG ATC GAT GAG GAC AGA GCG	280
Val Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala	
80 85 90	

## (2) INFORMATION FOR SEQ ID NO: 150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

```

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
 1             5             10             15
Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
          20             25             30
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
          35             40             45
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
          50             55             60
Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
          65             70             75             80
Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Arg Ala
          85             90

```

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 499 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..499

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA AAC ACC AAC      48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
 1             5             10             15
CGT CGC CCA CAG GAC GTC AAG TTC CCG GGC GGT GGT CAG ATC GTT GGC      96
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly
          20             25             30

```

GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG ATG GGT GTG CGC GCG 144  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala  
 35 40 45  
 ACT CGG AAG ACT TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG CCT 192  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 ATT CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA CCC GGG 240  
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly  
 65 70 75 80  
 TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC GGG TGG GCA GGG TGG 288  
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95  
 CTG CTC TCC CCT CGA GGC TCT CGG CCT AAT TGG GGC CCC AAT GAC CCC 336  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 CGG CGA AAA TCG CGT AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC 384  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 GGA TTC GCC GAT CTC ATG GGG TAT ATC CCG CTC GTA GGC GGC CCC ATT 432  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile  
 130 135 140  
 GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT GAG GAC 480  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 GGG GTA AAC TAT GCA ACA G 499  
 Gly Val Asn Tyr Ala Thr  
 165

## (2) INFORMATION FOR SEQ ID NO: 152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Met Gly Val Arg Ala  
 35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Gln Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly Pro Ile  
 130 135 140  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp  
 145 150 155 160  
 Gly Val Asn Tyr Ala Thr  
 165

## (2) INFORMATION FOR SEQ ID NO: 153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ACG TGC GGA TTC GCC GAT CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG GTC CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTA AAC TAT CCA ACA GGG AAT TTA CCC GGT TGC TCT TTC	144



Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 TCT ATC TTT ATT CTT GCT CTT CTC TCG TGT CTG ACC GTT CCG GCC TCT 192  
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 GCA GTT CCC TAC CGA AAT GCC TCT GGG ATT TAT CAT GTT ACC AAT GAT 240  
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT AAC CTG ATC CTA CAC 298  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His  
 85 90 95  
 GCA CCT GGT TGC GTG CCT TGT GTC ATG ACA GGT AAT GTG AGT AGA TGC 336  
 Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys  
 100 105 110  
 TGG GTC CAA ATT ACC CCT ACA CTG TCA GCC CCG AGC CTC GGA GCA GTC 384  
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val  
 115 120 125  
 ACG GCT CCT CTT CGG AGA GCC GTT GAC TAC CTA GCG GGA GGG GCT GCC 432  
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala  
 130 135 140  
 CTC TGC TCC GCG TTA TAC GTA GGA GAC GCG TGT GGG GCA CTA TTC TTG 480  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160  
 GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAC GCT ACG GTG CAG 528  
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175  
 AAC TGC AAC TGT TCC ATT TAC AGT GGC CAT GTT ACC GGC CAC CGG ATG 576  
 Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met  
 180 185 190  
 GCG 579  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Gly  
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu  
 20 25 30

Glu Asp Gly Val Asn Tyr Pro Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45

Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60

Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu His  
 85 90 95

Ala Pro Gly Cys Val Pro Cys Val Met Thr Gly Asn Val Ser Arg Cys  
 100 105 110

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu Gly Ala Val  
 115 120 125

Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala Gly Gly Ala Ala  
 130 135 140

Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175

Asn Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Arg Met  
 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 579 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC 48  
 Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly  
 1 5 10 15  
 CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT 96  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu  
 20 25 30  
 GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC 144  
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT 192  
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT 240  
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC 288  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His  
 85 90 95  
 GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC 336  
 Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys  
 100 105 110  
 TGG GTC CAA ATT ACC CCC ACG CTG TCA GCC CCG AGC TTC GGA GCA GTC 384  
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val  
 115 120 125  
 ACG GCT CCC CTT CGG AGA GCC GTT GAT TAC TTG GTG GGA GGG GCT GCC 432  
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala  
 130 135 140  
 CTC TGC TCC GCG TTA TAC GTT GGA GAC GCG TGT GGG GCA CTA TTT TTG 480  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160  
 GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAT GCT ACG GTG CAG 528  
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175  
 GAC TGC AAC TGT TCC ATC TAC AGT GGC CAC GTC ACC GGC CAT CAG ATG 576  
 Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met  
 180 185 190  
 GCA 579  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 156:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu  
 20 25 30  
 Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His  
 85 90 95  
 Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys  
 100 105 110  
 Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val  
 115 120 125  
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 157:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 3..530

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 3..527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CA CCT ACG ACA GCT CTG CTG GTG GCC CAG TTA CTG CGG ATT CCC CAA	47
Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln	
1 5 10 15	
GTG GTC ATT GAC ATC ATC GCA GGG AGC CAC TGG GGG GTC TTG TTT GCC	95
Val Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala	
20 25 30	
GCC GCA TAC TAT GCA TCG GTG GCT AAC TGG ACC AAG GTC GTG CTG GTC	143
Ala Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val	
35 40 45	
TTG TTT CTG TTT GCA GGG GTT GAT GCT ACT ACC CAG ATT TCG GGC GGC	191
Leu Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly	
50 55 60	
TCC AGC GCC CAA ACG ACG TAT GGC ATC GCC TCA TTT ATC ACC CGC GGC	239
Ser Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly	
65 70 75	
GCG CAG CAG AAA CTG CAG CTC ATA AAT ACC AAC GGA AGC TGG CAC ATC	287
Ala Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile	
80 85 90 95	
AAC AGG ACC GCC CTT AAT TGT AAT GAC AGC CTC CAG ACT GGG TTC ATA	335
Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile	
100 105 110	
GCC GGC CTC TTC TAC TAC CAT AAG TTC AAC TCT TCT GGA TGC CCG GAT	383
Ala Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp	
115 120 125	
CGG ATG GCT AGC TGT AGG GCC CTT GCC ACT TTT GAC CAG GGC TGG GGA	431
Arg Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly	
130 135 140	
ACT ATC AGC TAT GCC AAC ATA TCG GGT CCC AGT GAT GAC AAA CCA TAT	479
Thr Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr	
145 150 155	
TGC TGG CAC TAT CCC CCA CGG CCG TGC GGA GTG GTG CCA GCC CAA GAG	527

Cys Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu  
160 165 170 175

GTC  
Val

530

## (2) INFORMATION FOR SEQ ID NO: 158:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Pro Thr Thr Ala Leu Leu Val Ala Gln Leu Leu Arg Ile Pro Gln Val  
1 5 10 15  
Val Ile Asp Ile Ile Ala Gly Ser His Trp Gly Val Leu Phe Ala Ala  
20 25 30  
Ala Tyr Tyr Ala Ser Val Ala Asn Trp Thr Lys Val Val Leu Val Leu  
35 40 45  
Phe Leu Phe Ala Gly Val Asp Ala Thr Thr Gln Ile Ser Gly Gly Ser  
50 55 60  
Ser Ala Gln Thr Thr Tyr Gly Ile Ala Ser Phe Ile Thr Arg Gly Ala  
65 70 75 80  
Gln Gln Lys Leu Gln Leu Ile Asn Thr Asn Gly Ser Trp His Ile Asn  
85 90 95  
Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr Gly Phe Ile Ala  
100 105 110  
Gly Leu Phe Tyr Tyr His Lys Phe Asn Ser Ser Gly Cys Pro Asp Arg  
115 120 125  
Met Ala Ser Cys Arg Ala Leu Ala Thr Phe Asp Gln Gly Trp Gly Thr  
130 135 140  
Ile Ser Tyr Ala Asn Ile Ser Gly Pro Ser Asp Asp Lys Pro Tyr Cys  
145 150 155 160  
Trp His Tyr Pro Pro Arg Pro Cys Gly Val Val Pro Ala Gln Glu Val  
165 170 175

## (2) INFORMATION FOR SEQ ID NO: 159:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

C TCG ACC GTT ACC GAA CAT GAC ATA ATG ACC GAA GAG TCC ATT TAC	46
Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CAA TCA TGT GAC TTG CAG CCC GAG GCA CGC GCA GCA ATA CGG TCA CTC	94
Gln Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu	
20 25 30	
ACC CAA CGC CTC TAC TGT GGA GGC CCC ATG TAC AAC AGC AAG GGG CAA	142
Thr Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln	
35 40 45	
CAG TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTT TTC ACC ACC AGT	190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGC AAC ACC ATG ACG TGC TAC ATC AAG GCT TTA GCC TCC TGT AGA	238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg	
65 70 75	
GCC GCA AGG CTC CGG GAC TGC ACG CTC CTG GTG TGT GGT GAC GAT CTT	286
Ala Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCA AGC CTG	334
Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu	
100 105 110	
AGA GCC	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Ser Thr Val Thr Glu His Asp Ile Met Thr Glu Glu Ser Ile Tyr Gln  
 1 5 10 15

Ser Cys Asp Leu Gln Pro Glu Ala Arg Ala Ala Ile Arg Ser Leu Thr  
 20 25 30

Gln Arg Leu Tyr Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln  
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met  
 50 55 60

Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg Ala  
 65 70 75 80

Ala Arg Leu Arg Asp Cys Thr Leu Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Ser Leu Arg  
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

C TCA ACC GCC ACC GAA CAT GAC ATA TTG ACT GAA GAG TCC ATA TAC  
 Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr

46



1	5	10	15	
CAA TCA TGT GAC TCG CAG CCC GAC GCA CGC GCA GCA ATA CGG TCA CTC				94
Gln Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu				
	20	25	30	
ACC CAA CGC TTG TTC TGT GGA GGC CCC ATG TAT AAC AGC AAG GGG CAA				142
Thr Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln				
	35	40	45	
CAA TGT GGT TAT CGC AGA TGC CGC GCC AGC GGC GTC TTC ACC ACC AGT				190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser				
	50	55	60	
ATG GGC AAC ACC ATG ACG TGC TAC ATT AAG GCT TTA GCC TCC TGT AGA				238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ser Cys Arg				
	65	70	75	
ACC GCT GGG CTC CGG GAC TAC ACG CTC CTG GTG TGT GGT GAC GAT CAT				286
Thr Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His				
	80	85	90	95
GTG GCC ATC TGC GAG AGC CAG GGG ACA CAC GAG GAT GAA GCG AAC CTG				334
Val Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu				
	100	105	110	
AGA GCC				340
Arg Ala				

## (2) INFORMATION FOR SEQ ID NO: 162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ser Thr Ala Thr Glu His Asp Ile Leu Thr Glu Glu Ser Ile Tyr Gln				
1	5	10	15	
Ser Cys Asp Ser Gln Pro Asp Ala Arg Ala Ala Ile Arg Ser Leu Thr				
	20	25	30	
Gln Arg Leu Phe Cys Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Gln				
	35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met				
	50	55	60	
Gly Asn Thr Met Thr Cys Tyr Ile-Lys Ala Leu Ala Ser Cys Arg Thr				
	65	70	75	80
Ala Gly Leu Arg Asp Tyr Thr Leu Leu Val Cys Gly Asp Asp His Val				
	85	90	95	

Ala Ile Cys Glu Ser Gln Gly Thr His Glu Asp Glu Ala Asn Leu Arg  
 100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 163:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 499 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..499

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGC ACG AAT CCT AAA CTT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGT GGT GGC CAG ATC GTT GGC	96
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCT AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGG CGC CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCG CGC CGA TCC GAG GGC AGA TCC TGG GCG CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	
65 70 75 80	
TAT CCT TGG CCC CTT TAC GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCC CCT CGC GGG TCT CGG CCG TCT TGG GGC CCT AAT GAT CCC	336

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro  
 100 105 110  
 CGG CGG AGG TCC CGC AAC CTG GGT AAG GTC ATC GAT ACC CTA ACA TGC 384  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC CCC GTG 432  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val  
 130 135 140  
 GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG GAA GAC 480  
 Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
 145 150 155 160  
 GGG ATC AAC TAC GCA ACA G 499  
 Gly Ile Asn Tyr Ala Thr  
 165

## (2) INFORMATION FOR SEQ ID NO: 164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Met Ser Thr Asn Pro Lys Leu Gln Arg Lys Thr Lys Arg Asn Thr Asn  
 1 5 10 15  
 Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45  
 Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro  
 100 105 110  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Val  
 130 135 140

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
 145 150 155 160

Gly Ile Asn Tyr Ala Thr  
 165

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCTATG	60
GACGTTAAGT TCCCAGGCCG TGGTCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG	180
AGGCGCCAAC CTATCCCCAA GCGCGCCCGA ACCGAGGGCA GATCCTGGGC GCAGCCCCGG	240
TATCCTTGGC CCCTTTACGG CAATGAGGGC TGTGGGTGGG CAGGGTGGCT CCTGTCCCCCT	300
CGCGNTCTC GGNCGTCTTG GGGCCCCAAT GATCCCCGNN GGAGATCCCG CAACTTGGGT	360
AAGGTCATCG ATACCCTAAC ATGCGGCTTC GCCGACCTCA TGGGATACAT CCCGCTTGTA	420
GGCGCCCCCG TGGGTGGCGT CGCCAGGGCC CTGGCACATG GTGTTAGGGC TGTGGAAGAC	480
GGGATCAATT ATGCAACAG	499

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn

1	5	10	15
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Ala Arg Arg Thr Glu Gly Arg Ser Trp Ala Gln Pro Gly			
65	70	75	80
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp			
85	90	95	
Leu Leu Ser Pro Arg Xaa Ser Arg Xaa Ser Trp Gly Pro Asn Asp Pro			
100	105	110	
Arg Xaa Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu			
115	120	125	

## (2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGG GCC-CTG GCA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATC AAT TAT GCA ACA GGG AAC CTT CCC GGT TGC TCC TTT	144

Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	
		35					40					45				
TCT	ATC	TTC	CTC	TTG	GCG	CTC	CTC	TCG	TGC	CTG	ACT	GTT	CCC	ACA	TCG	192
Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Thr	Ser	
		50				55				60						
GCC	GTT	AAC	TAT	CGC	AAT	GCT	TCG	GGC	ATT	TAT	CAC	ATC	ACC	AAT	GAC	240
Ala	Val	Asn	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp	
		65			70				75					80		
TGC	CCG	AAT	GCA	AGC	ATA	GTG	TAC	GAG	ACC	GAA	AAT	CAC	ATC	TTA	CAC	288
Cys	Pro	Asn	Ala	Ser	Ile	Val	Tyr	Glu	Thr	Glu	Asn	His	Ile	Leu	His	
				85				90						95		
CTC	CCA	GGG	TGC	GTA	CCC	TGT	GTG	AGG	ACT	GGG	AAC	CAG	TCG	CGG	TGT	336
Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Thr	Gly	Asn	Gln	Ser	Arg	Cys	
				100				105					110			
TGG	GTG	GCC	CTC	ACT	CCC	ACA	GTA	GCG	TCG	CCA	TAC	GCC	GGT	GCT	CCG	384
Trp	Val	Ala	Leu	Thr	Pro	Thr	Val	Ala	Ser	Pro	Tyr	Ala	Gly	Ala	Pro	
		115					120					125				
CTT	GAG	CCC	TTG	CGG	CGT	CAT	GTG	GAC	CTG	ATG	GTA	GGT	GCT	GCC	ACC	432
Leu	Glu	Pro	Leu	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr	
		130				135					140					
ATG	TGT	TCC	GCC	CTC	TAC	ATC	GGC	GAC	TTG	TGC	GGT	GGC	TTA	TTC	TTG	480
Met	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Leu	Cys	Gly	Gly	Leu	Phe	Leu	
		145			150				155					160		
GTG	GGC	CAA	ATG	TTC	ACC	TTC	CAA	CCG	CGA	CGT	CAC	TGG	ACC	ACT	CAG	528
Val	Gly	Gln	Met	Phe	Thr	Phe	Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	
				165				170					175			
GAC	TGC	AAT	TGT	TCC	ATC	TAC	ACG	GGC	CAC	ATT	ACG	GGT	CAT	CGG	ATG	576
Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly	His	Ile	Thr	Gly	His	Arg	Met	
			180					185					190			
GCA																579
Ala																

## (2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala
1						5				10				15	

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
 50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His  
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys  
 100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro  
 115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 169:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATC AAC TAC GCA ACA GGG AAT CTC CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GCA CTT CTC TCG TGC CTC ACT GTT CCC GCG TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GGC GTT AAC TAT CGC AAT GCT TCG GGC GTT TAT CAC ATC ACC AAC GAC	240
Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT GCG AGC ATA GTG TAC GAG ACC GAC AAT CAC ATC TTA CAC	288
Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His	
85 90 95	
CTC CCA GGG TGC GTA CCC TGT GTG AAG ACC GGG AAC CAG TCG CGG TGT	336
Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC ACT CCC ACA GTG GCG TCG CCT TAC GTC GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro	
115 120 125	
CTC GAG CCC TTG CGG CGC CAT GTG GAC CTG ATG GTA GGT GCT GCC ACC	432
Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
GTG TGC TCC GCC CTC TAC GTC GGC GAC CTG TGC GGT GGC TTA TTC TTG	480
Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TTC CAA CCG CGA CGC CAC TGG ACG ACC CAG	528
Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAC TGT AAT TGT TCC ATC TAC GCA GGG CAT ATT ACG GGC CAT CGG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met	
180 185 190	
GCT	579
Ala	

(2) INFORMATION FOR SEQ ID NO: 170:



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Gly Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Asp Asn His Ile Leu His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys  
 100 105 110  
 Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Val Gly Ala Pro  
 115 120 125  
 Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

(2) INFORMATION FOR SEQ ID NO: 171:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..579

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

ACA TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTT GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTT GGT GGC GTC GCC AGA GCC CTT GCG CAC GGC GTC AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAA GAC GGG ATT AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAC CAC CTC ACC AAT GAC	240
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp	
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GTC CAT CAC ATC TTG CAC	288
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His	
85 90 95	
CTT CCA GGA TGC GTC CCT TGT GTA AGA ACT GGG AAC CAG TCT CGG TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTA GCC TTG ACC CCC ACG CTG GCC GCG CCA TAC CTT GGC GCT CCA	384
Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro	
115 120 125	
CTC GAG TCC ATG CGG CGT CAC GTG GAT TTG ATG GTG GGC ACT GCT ACA	432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr	
130 135 140	
TTG TGC TCA GCA CTC TAC GTT GGG GAC CTG TGC GGG GGC ATA TTC CTA	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu	
145 150 155 160	
GCG GGC CAG ATG TTC ACC TTC CGG CCC CGC CTC CAT TGG ACC ACC CAG	528
Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln	
165 170 175	

T05090" 422E2860

GAG TGC AAT TGT TCC ACC TAT CCG GGC CAC ATC ACG GGT CAT AGA ATG 576  
 Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met  
 180 185 190

GCG 579  
 Ala

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Leu Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Val His His Ile Leu His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys  
 100 105 110  
 Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro Tyr Leu Gly Ala Pro  
 115 120 125  
 Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ile Phe Leu  
 145 150 155 160  
 Ala Gly Gln Met Phe Thr Phe Arg Pro Arg Leu His Trp Thr Thr Gln  
 165 170 175  
 Glu Cys Asn Cys Ser Thr Tyr Pro Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 173:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

ACG TGC GGT TCC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCG CAT GGC GTC AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATA AAC TAT GCA ACA GGG AAC CTT CCT GGT TGC TCT TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTG GCA CTT CTC TCG TGC CTG ACT GTC CCC GCC TCA	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCT GTG CAT TAT CAC AAC ACC TCG GGC ATC TAT CAC ATC ACT AAT GAC	240
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCT AAC TCT AGC ATA GTC TTT GAG GCA GAG CAT CAC ATC TTG CAT	288
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His	
85 90 95	
CTT CCA GGA TGC GTC CCC TGT GTG AGA ACT GGG AAC CAG TCA CGA TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG ATA GCC TTG ACC CCT ACG TTG GCC GCG CCA CAC ATT GGC GCT CCA	384
Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro	

115	120	125	
CTT GAG TCC ATG CGA CGT CAT GTG GAT TTG ATG GTA GGC ACT GCC ACA			432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr			
130	135	140	
TTG TGC TCC GCA CTC TAC ATT GGA GAT CTG TGC GGA GGC ATA TTT CTA			480
Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu			
145	150	155	160
GTG GGC CAG ATG TTC AAC TTC AGG CCC CGC CTG CAC TGG ACC ACC CAG			528
Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln			
165	170	175	
GAG TGC AAT TGT TCC ATC TAT CCA GGC CAC ATC ACG GGT CAC AGA ATG			576
Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met			
180	185	190	
GCG			579
Ala			

## (2) INFORMATION FOR SEQ ID NO: 174:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Thr Cys Gly Ser Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala		
1	5	10 15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val		
20	25	30
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe		
35	40	45
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser		
50	55	60
Ala Val His Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp		
65	70	75 80
Cys Pro Asn Ser Ser Ile Val Phe Glu Ala Glu His His Ile Leu His		
85	90	95
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys		
100	105	110
Trp Ile Ala Leu Thr Pro Thr Leu Ala Ala Pro His Ile Gly Ala Pro		
115	120	125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Thr Ala Thr  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ile Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Asn Phe Arg Pro Arg Leu His Trp Thr Thr Gln  
 165 170 175  
 Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 175:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

ACG TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC TTG GCA CAT GGT GTC AGG GCC GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATT AAC TAT GCA ACA GGG AAT CTT CCC GGT TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTT CTA GCA CTT CTC TCG TGC TTG ACT GTC CCG GCC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu-Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCG CAG CAC TAC CGG AAC ATC TCG GGC ATT TAT CAC GTC ACC AAT GAC	240
Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp	

65	70	75	80	
TGC CCG AAC TCT AGT ATA GTG TAT GAA GCT GAC CAT CAT ATC ATG CAT				288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His				
	85	90	95	
CTA CCA GGG TGT GTG CCT TGC GTG AGA ACC GGG AAC ACC TCG CGC TGC				336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys				
	100	105	110	
TGG GTT CCT TTA ACA CCC ACT GTG GCT GCC CCC TAT GTT GGC GCG CCG				384
Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro				
	115	120	125	
CTC GAA TCC ATG CGG CGG CAC GTG GAC TTA ATG GTG GGT GCC GCC ACC				432
Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr				
	130	135	140	
GTC TGC TCG GCC CTG TAC ATC GGA GAC CTT TGC GGA GGT GTC TTC CTG				480
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu				
	145	150	155	160
GTC GGG CAG ATG TTC ACC TTC CGG CCG CGC CGC CAT TGG ACT ACC CAG				528
Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln				
	165	170	175	
GAC TGC AAC TGC TCT ATC TAT GAT GGC CAC ATC ACC GGC CAT AGA ATG				576
Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met				
	180	185	190	
GCT				579
Ala				

## (2) INFORMATION FOR SEQ ID NO: 176:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala			
1	5	10	15
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val			
	20	25	30
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe			
	35	40	45
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser			
	50	55	60

Ala Gln His Tyr Arg Asn Ile Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Thr Ser Arg Cys  
 100 105 110

Trp Val Pro Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro  
 115 120 125

Leu Glu Ser Met Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Thr Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Asp Gly His Ile Thr Gly His Arg Met  
 180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 579 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..579
- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ACG TGC GGG TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCT 48  
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15

CCA GTA GGA GGC GTC GCC AGA GCC TTG GCG CAT GGC GTC AGG GCT GTG 96  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val



20

25

30

GAG GAC GGG ATC AAT TAC GCA ACA GGG AAC CTT CCC GGC TGC TCC TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GTA CTT CTC TCG CGC CTA ACT GTC CCA GCG TCT	192
Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser	
50 55 60	
GCT CAG CAC TAC CGG AAT GCA TCG GGC ATC TAC CAT GTC ACC AAC GAC	240
Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCC AGT ATT GTG TAT GAA GCC GAC CAT CAC ATC ATG CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His	
85 90 95	
CTA CCC GGG TGT GTG CCC TGT GTA AGA ACT GGG AAT GTC TCG CGT TGC	336
Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys	
100 105 110	
TGG ATT CCT TTA ACA CCC ACT GTA GCC GTC CCC TAC CTC GGG GCT CCA	384
Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro	
115 120 125	
CTT ACG TCT GTA CGG CAG CAT GTG GAC CTG ATG GTG GGG GCG GCC ACC	432
Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr	
130 135 140	
TTA TGC TCT GCC CTC TAC ATC GGA GAC CAT TGC GGA GGT GTC TTC TTG	480
Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu	
145 150 155 160	
GCA GGG CAG ATG GTC AGT TTC CAA CCC CGG CGT CAT TGG ACT ACC CAG	528
Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln	
165 170 175	
GAT TGC AAC TGT TCC ATC TAT GTG GGC CAC ATC ACC GGC CAC AGG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met	
180 185 190	
GCC	576
Ala	

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Val Leu Leu Ser Arg Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Ile Pro Leu Thr Pro Thr Val Ala Val Pro Tyr Leu Gly Ala Pro  
 115 120 125  
 Leu Thr Ser Val Arg Gln His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Ile Gly Asp His Cys Gly Gly Val Phe Leu  
 145 150 155 160  
 Ala Gly Gln Met Val Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 179:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

ACCTGCGGGCT TCGCCGACCT CATGGGATAC ATCCCGCTCG TAGGCGCCCC CGTGGGAGGC 60  
 GTCGCCAGAR CTCTGGCGCA TGGCTCAGG GCTCTGGAAG ACGGGATCAA TTATGCAACA 120  
 GGGAAATCTTC CTGGTTGCTC TTTCTCTATC TCCCTTCTTG AACTTCTCTC GTGCCTGACT 180  
 GTTCCCGCCT CAGCCATCCA CTATCGCAAT GCTTCGGACG GTTATTATAT CACCAATGAT 240  
 TGCCCGAACT CTAGCATAGT GTATGAAGCC GAGAACCACA TCTTGACACT TCCGGGGTGT 300  
 ATACCCTGTG TGAAGACCGG GAATCAGTCG CGGTGCTGGG TGGCTCTCAC CCCCACGCTG 360  
 GCGGCCCCAC ACCTACGTGC TCCGCTTTCG TCCTTACGGG CGCATGTGGA CCTAATGGTG 420  
 GGGGCCGCCA CGGCATGCTC CGCTTTTAC ATTGGAGATC TGTGCGGGGG TGTGTTTTTG 480  
 GCGGGCCAAC TGTTCACTAT CCGGCCACGC ATTCATGAAA CCACTCAGGA CTGCAATTGC 540  
 TCCATCTACT CAGGGCACAT CACGGGTNNN NNNNNNNN 579

## (2) INFORMATION FOR SEQ ID NO: 180:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Xaa Leu Ala His Gly Val Arg Ala Leu  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Ser Leu Leu Glu Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Glu Asn His Ile Leu His  
 85 90 95  
 Leu Pro Gly Cys Ile Pro Cys Val Lys Thr Gly Asn Gln Ser Arg Cys  
 100 105 110

Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Pro His Leu Arg Ala Pro  
 115 120 125  
 Leu Ser Ser Leu Arg Ala His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Ala Cys Ser Ala Phe Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160  
 Ala Gly Gln Leu Phe Thr Ile Arg Pro Arg Ile His Glu Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly Xaa Xaa Xaa  
 180 185 190  
 Xaa

## (2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..578

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

GCGTGCGGCT TCGCCGATCT CATGGGATAC ATCCCGCTCG TAGGCGCCCC CGTGGGTGGC	60
GTCGCCAGAG CCCTGGCGCA CGGTGTTAGG GCTGTGGAGG ACGGGATTAA CTACGCAACA	120
GGGAATCTTC CTGGTTGCTC TTTCTCTATC TNCCTTCTGG CACTTCTCTC GTGCCTGACT	180
GTCCCGGCCCT CGGCTCAGCA CTACCGGAAT GTCTCGGGCA TCTACCACGT CACCAATGAT	240
TGCCCCGAATT CCAGCATAGT GTATGAAGCC GATCACCACA TCATGCACTT ACCAGGGTGC	300
ATACCCTGCG TGAGGACCGG GAACGTTTCG CGCTGCTGGG TATCTCTGAC ACCTACTGTG	360
GCTGCTCCCT ACCTCGGGGC TCCGCTTACG TCGCTACGGC GGCATGTGGA TTTGATGGTG	420
GGTGCGACCA CCCTTTGCTC TGCCCTCTAC GTCGGAGACC TCTGTGGAGG TGTCTTCCTA	480

GTGGGACAGA TGTTCACCTT CCAGCCGCGC CGCCACTGGA CCACTCAGGA CTGCAACTGC 540  
 TCCATTTACG TCGGCCACAT CACAGGCCAC AGAATGGCT 579

## (2) INFORMATION FOR SEQ ID NO: 182:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Xaa Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Met His  
 85 90 95  
 Leu Pro Gly Cys Ile Pro Cys Val Arg Thr Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Val Ser Leu Thr Pro Thr Val Ala Ala Pro Tyr Leu Gly Ala Pro  
 115 120 125  
 Leu Thr Ser Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Val Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 183:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..579

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

ACC TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTA GAA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGT ATT AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTT	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TCC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCA	192
Ser Ile Ser Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC GTC AAC TAT CGC AAC GCC TCG GGC GTC TAT CAT ATC ACC AAT GAC	240
Ala Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp	
65 70 75 80	
TGC CCG AAT TCG AGC ATA GTG TAC GAG GCT GAC TAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Tyr His Ile Leu His	
85 90 95	
CTC CCT GGG TGC TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTT ACT CCC ACC GTG GCG GCG CCT TAC GTT GGT GCT CCG	384
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Val Gly Ala Pro	

115

120

125

CTA GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCT GCT ACT  
 Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140

GTG TGC TCC GCT CTT TAC ATC GGG GAC CTG TGC GGT GGC GTA TTT TTG  
 Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160

GTT GGT CAG ATG TTT TCT TTC CAG CCG CGA CGC CAC TGG ACC ACG CAG  
 Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

GAC TGC AAT TGT TCT ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG  
 Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met  
 180 185 190

5.

576

579

GCA  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
 50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80

Cys Pro Asn Ala Ser Ile Val Tyr Glu Thr Glu Asn His Ile Leu His  
 85 90 95

Leu Pro Gly Cys Val Pro Cys Val Arg Thr Gly Asn Gln Ser Arg Cys  
 100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ser Pro Tyr Ala Gly Ala Pro  
 115 120 125

Leu Glu Pro Leu Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140

Met Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Leu Phe Leu  
145 150 155 160

Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Ala Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
35 40 45

Ser Ile Ser Phe Trp His Phe Ser Arg Ala \* Leu Ser Arg Pro Arg  
50 55 60

Leu Ser Thr Thr Gly Met Ser Arg Ala Ser Thr Thr Ser Pro Met Ile  
65 70 75 80

Ala Arg Ile Pro Ala \* Cys Met Lys Pro Ile Thr Thr Ser Cys Thr  
85 90 95

Tyr Gln Gly Ala Tyr Pro Ala \* Gly Pro Gly Thr Phe Arg Ala Ala  
100 105 110

Gly Tyr Leu \* His Leu Leu Trp Leu Leu Pro Thr Ser Gly Leu Arg  
115 120 125

Leu Arg Arg Tyr Gly Gly Met Trp Ile \* Trp Trp Val Gln Pro Pro  
130 135 140

Phe Ala Leu Pro Ser Thr Ser Glu Thr Ser Val Glu Val Ser Ser \*  
145 150 155 160

Trp Asp Arg Cys Ser Pro Ser Ser Arg Ala Ala Thr Gly Pro Leu Arg  
165 170 175

Thr Ala Thr Ala Pro Phe Thr Ser Ala Thr Ser Gln Ala Thr Glu Trp



180

185

190

## (2) INFORMATION FOR SEQ ID NO: 185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC	240
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His	
85 90 95	
CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT	336
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys	
100 105 110	
TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA	384

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
 115 120 125

GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT 432  
 Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr  
 130 135 140

GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GTA TTC TTG 480  
 Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160

GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG 528  
 Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG 576  
 Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met  
 180 185 190

GCA 579  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 193 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val  
 20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
 50 55 60

Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp  
 65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His  
 85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
 100 105 110

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
 115 120 125

Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr  
 130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
 145 150 155 160

Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met  
 180 185 190

Ala

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCT GTG GGT GGC GTC GCC AGG GCC CTG GCA CAC GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGG ATC AAT TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC CTC TTG GCA CTT CTT TCG TGC CTG ACT GTT CCC ACC TCG	192
Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser	
50 55 60	
GCC GTC AAC TAT CGC AAT GCC TCG GGC ATC TAT CAC ATC ACC AAT GAC	240

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
65 70 75 80

TGC CCG AAC TCG AGC ATA GTG TAC GAG ACC GAG CAC CAC ATC CTA CAC  
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His  
85 90 95

CTC CCA GGG TGT TTA CCC TGC GTG AGG GTT GGG AAT CAG TCA CGC TGC  
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

TGG GTG GCC CTC ACT CCC ACC GTG GCG GCG CCT TAC ATC GGC GCT CCG 381  
Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

CTT GAA TCC CTC CGG AGT CAT GTG GAT CTG ATG GTA GGT GCC GCT ACT 432  
Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr  
130 135 140

GCG TGC TCC GCT CTT TAC ATC GGA GAC CTG TGC GGT GGC GTA TTT TTG 480  
Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

GTT GGT CAG ATG TTC TCT TTC CAG CCG CGG CGC CAC TGG ACT ACG CAG 528  
Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC GTT ACG GGC CAC AGG ATG 576  
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met  
180 185 190

GCA 579  
Ala

## (2) INFORMATION FOR SEQ ID NO: 188:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
35 40 45

Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
50 55 60

Ala Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Glu His His Ile Leu His  
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

Leu Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr  
130 135 140

Ala Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

Val Gly Gln Met Phe Ser Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Val Thr Gly His Arg Met  
180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

ACG TGC GGC TTC GCC GAC CTC ATG GGA TAC ATC CCG CTC GTG GGC GCC  
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
1 5 10 15

48

CCC GTT GGG GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG GCT GTG 96  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30

GAG GAC GGG ATT AAC TAT GCG ACA GGG AAT CTT CCC GGT TGC TCT TTC 144  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45

TCT ATC TTC CTC CTG GCA CTT CTT TCG TGC CTC ACT GTC CCA GCG TCA 192  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60

GCT GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC AAT GAC 240  
 Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80

TGT CCG AAT TCC AGC GTA GTC TAT GAA ACT GAC CAC CAT ATA TTG CAC 288  
 Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His  
 85 90 95

TTG CCG GGG TGC GTA CCC TGC GTG AGG GCC GGG AAC GTG TCT CGT TGC 336  
 Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys  
 100 105 110

TGG ACG CCG GTA ACA CCT ACG GTG GCT GCC GTA TCC ATG GAC GCT CCG 384  
 Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro  
 115 120 125

CTC GAG TCC TTC CGG CGG CAT GTG GAC CTA ATG GTA GGT GCG GCC ACC 432  
 Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140

GTG TGT TCT GTC CTC TAT GTT GGA GAC CTC TGT GGA GGT GCT TTC CTA 480  
 Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu  
 145 150 155 160

GTG GGG CAG ATG TTC ACC TTC CAG CCG CGT CGC CAC TGG ACC ACG CAG 528  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175

GAT TGT AAT TGC TCC ATC TAT ACT GGC CAT ATC ACC GGC CAC AGG ATG 576  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
 180 185 190

GCG 579  
 Ala

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
 1 5 10 15  
 Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val  
 20 25 30  
 Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe  
 35 40 45  
 Ser Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser  
 50 55 60  
 Ala Glu His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile Thr Asn Asp  
 65 70 75 80  
 Cys Pro Asn Ser Ser Val Val Tyr Glu Thr Asp His His Ile Leu His  
 85 90 95  
 Leu Pro Gly Cys Val Pro Cys Val Arg Ala Gly Asn Val Ser Arg Cys  
 100 105 110  
 Trp Thr Pro Val Thr Pro Thr Val Ala Ala Val Ser Met Asp Ala Pro  
 115 120 125  
 Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr  
 130 135 140  
 Val Cys Ser Val Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Thr Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Thr Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 1..289

## (ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..286

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCC ATG GAC GTT AAG TTC CCG GGC GGT GGC CAG ATC GTT GGT	96
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC AGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT AGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGG AGA CGT CAG CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAG CCC GGG	240
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	
65 70 75 80	
TAC CCA TGG CCT CTT TAC GGT AAT GAG GGT TGT GGG TGG GCA GGA TGG G	289
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	

## (2) INFORMATION FOR SEQ ID NO: 192:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly	



65

70

75

80

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
85 90 95

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..498

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT AAC ACC AAC	48
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1 5 10 15	
CGC CGC CCT ATG GAC GTA AAG TTC CCG GGC GGT GGA CAG ATC GTT GGC	96
Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20 25 30	
GGA GTT TAC TTG TTG CCG CGC AGG GGC CCC CGG TTG GGT GTG CGC GCG	144
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	
35 40 45	
ACT CGG AAG ACT TCG GAG CGG TCG CAA CCT CGT GGC AGG CGT CAA CCT	192
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro	
50 55 60	
ATC CCC AAG GCG CGC CGG TCC GAG GGC AGG TCC TGG GCG CAA GCC GGG	240
Ile Pro Lys Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln Ala Gly	
65 70 75 80	
TAC CCC TGG CCC CTC TAT GGC AAT GAG GGC TGT GGG TGG GCA GGG TGG	288
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp	
85 90 95	
CTC CTG TCT CCT CGC GGC TCT CGG CCA TCT TGG GGC CCA AAT GAT CCC	336

Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro		
			100					105					110				
CGG	CGG	AGA	TCG	CGC	AAT	CTG	GGT	AAG	GTC	ATC	GAT	ACC	CTG	ACG	TGC		384
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys		
		115					120					125					
GGC	TTC	GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	CTC	GTG	GGC	GCC	CCC	GTC		432
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Val		
	130					135					140						
GGG	GGC	GTC	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	AGG	GCT	GTG	GAG	GAC		480
Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Ala	Val	Glu	Asp		
145					150					155				160			
GGG	ATT	AAC	TAT	CGA	CAG												498
Gly	Ile	Asn	Tyr	Arg	Gln												
					165												

## (2) INFORMATION FOR SEQ ID NO: 194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn		
1				5					10					15			
Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly		
			20					25					30				
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala		
	35					40						45					
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro		
	50					55					60						
Ile	Pro	Lys	Ala	Arg	Arg	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Ala	Gly		
	65				70					75				80			
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp		
			85						90					95			
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro		
			100					105					110				
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys		
		115					120					125					
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Val		
	130					135						140					

Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Ala Val Glu Asp  
 145 150 155 160

Gly Ile Asn Tyr Arg Gln  
 165

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 579 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..579

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

ACG TGC GGA TTC GCC GAC CTC GTG GGG TAC ATC CCG CTC GTA GGC GGC	48
Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
CCC GTT GGG GGC GTC GCA AGG GCT CTC GCA CAT GGT GTG AGG GTT CTT	96
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
GAG GAC GGG GTG AAT TAT GCA ACA GGG AAT CTG CCT GGT TGC TCT TTC	144
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TTC ATT CTT GCA CTT CTC TCG TGC CTC ACT GTC CCG GCC TCT	192
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
GCA GTT CCC TAC CGA AAT GCC TCT GGG ATC TAT CAT GTC ACC AAT GAT	240
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
TGC CCA AAC TCT TCC ATA GTC TAT GAG GCA GAT GAT CTG ATC CTA CAC	288
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	
85 90 95	
GCA CCT GGC TGC GTG CCT TGT GTC AGG AAA GAT AAT GTG AGT AGG TGC	336

Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys	
100 105 110	
TGG GTC CAA ATT ACC CCC ACG CTG TCA GCC CCG AGC TTC GGA GCA GTC	384
Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val	
115 120 125	
ACG GCT CCC CTT CGG AGA GCC GTT GAT TAC TTG GTG GGA GGG GCT GCC	432
Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala	
130 135 140	
CTC TGC TCC GCG TTA TAC GTT GGA GAC GCG TGT GGG GCA CTA TTT TTG	480
Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu	
145 150 155 160	
GTA GGC CAA ATG TTC ACC TAT AGG CCT CGC CAG CAT GCT ACG GTG CAG	528
Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln	
165 170 175	
GAC TGC AAC TGT TCC ATC TAC AGT GGC CAC GTC ACC GGC CAT CAG ATG	576
Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met	
180 185 190	
GCA	579
Ala	

## (2) INFORMATION FOR SEQ ID NO: 196:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Thr Cys Gly Phe Ala Asp Leu Val Gly Tyr Ile Pro Leu Val Gly Gly	
1 5 10 15	
Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly Val Arg Val Leu	
20 25 30	
Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
Ser Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser	
50 55 60	
Ala Val Pro Tyr Arg Asn Ala Ser Gly Ile Tyr His Val Thr Asn Asp	
65 70 75 80	
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu His	
85 90 95	
Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser Arg Cys	
100 105 110	

Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Phe Gly Ala Val  
 115 120 125  
 Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Val Gly Gly Ala Ala  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys Gly Ala Leu Phe Leu  
 145 150 155 160  
 Val Gly Gln Met Phe Thr Tyr Arg Pro Arg Gln His Ala Thr Val Gln  
 165 170 175  
 Asp Cys Asn Cys Ser Ile Tyr Ser Gly His Val Thr Gly His Gln Met  
 180 185 190  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 579 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..579

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

ACT TGC GGC TTT GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC	48
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala	
1 5 10 15	
CCC GTG GGT GGC GTC GCC AGA GCC CTG GAA CAT GGT GTT AGG GCT GTG	96
Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val	
20 25 30	
GAG GAC GGC ATC AAT TAT GCA ACA GGG AAT CTC CCC GGT TGC TCT TTC	144
Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe	
35 40 45	
TCT ATC TAC CTC TTG GCA CTT CTC TCG TGC CTG ACT GTT CCC ACC TCG	192

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
50 55 60

GCC ATC CAC TAT CGC AAT GCC TCG GGC GTC TAC CAC GTC ACC AAT GAC 240  
Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp  
65 70 75 80

TGC CCG AAC TCG AGC ATA GTG TAC GAG GCC GAC CAC CAC ATC CTA CAC 288  
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His  
85 90 95

CTT CCA GGG TGC TTA CCC TGT GTG AGG GTT GGG AAT CAG TCA CGT TGT 336  
Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

TGG GTG GCC CTC TCT CCC ACC GTG GCG GCG CCT TAC ATC GGT GCT CCA 384  
Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

GTT GAA TCC TTC CGG AGA CAC GTG GAC ATG ATG GTG GGC GCT GCT ACT 432  
Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr  
130 135 140

GTG TGC TCC GCT CTC TAT ATT GGG GAC TTG TGT GGT GGC GTA TTC TTG 480  
Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

GTT GGT CAG ATG TTT TCT TTC CGG CCA CGA CGC CAC TGG ACT ACG CAG 528  
Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

GAC TGC AAT TGT TCC ATC TAC GCG GGG CAC ATC ACT GGC CAC GGA ATG 576  
Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met  
180 185 190

GCA 579  
Ala

## (2) INFORMATION FOR SEQ ID NO: 198:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala  
1 5 10 15

Pro Val Gly Gly Val Ala Arg Ala Leu Glu His Gly Val Arg Ala Val  
20 25 30

Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe

35

40

45

Ser Ile Tyr Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Thr Ser  
50 55 60

Ala Ile His Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp  
65 70 75 80

Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His  
85 90 95

Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser Arg Cys  
100 105 110

Trp Val Ala Leu Ser Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro  
115 120 125

Val Glu Ser Phe Arg Arg His Val Asp Met Met Val Gly Ala Ala Thr  
130 135 140

Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu  
145 150 155 160

Val Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln  
165 170 175

Asp Cys Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Gly Met  
180 185 190

Ala

## (2) INFORMATION FOR SEQ ID NO: 199:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1470

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..1467

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

A TCA CCA CCG GAG CTT CTA TCA CAT ACT CCA CTT ACG GCA AGT TCC  
Ser Pro Pro Glu Leu Leu Ser His Thr Pro Leu Thr Ala Ser Ser  
1 5 10 15

TTG CTG ATG GAG GGT GTT CAG GCG GCG CGC ATG ACG TGA TCA TAT GCG  
Leu Leu Met Glu Gly Val Gln Ala Ala Arg Met Thr \* Ser Tyr Ala

ACG	AGT	GCC	ATT	CCC	AGG	ACG	CCA	CCA	CCA	TTC	TTG	GGA	TAG	GCA	CTG
Thr	Ser	Ala	Ile	Pro	Arg	Thr	Pro	Pro	Pro	Phe	Leu	Gly	*	Ala	Leu
			35					40						45	

TCC TTG ACC AGG CAG AGA CGG CTG GAG CTA GGC TCG TCG TCT TGG CCA 190  
Ser Leu Thr Arg Gln Arg Arg Leu Glu Leu Gly Ser Ser Ser Trp Pro  
50 55 60

CGG CCA CCC CTC CCG GCA GTG TGA CAA CGC CCC ACC CCA ACA TCG AGG 238  
Arg Pro Pro Leu Pro Ala Val \* Gln Arg Pro Thr Pro Thr Ser Arg  
65 70 75

AAG TGG CCC TGC CTC AGG AGG GGG AGG TTC CCT TCT ACG GCA GAG CCA 286  
Lys Trp Pro Cys Leu Arg Arg Gly Arg Phe Pro Ser Thr Ala Glu Pro  
80 85 90 95

TTC CCC TTG CTT TTA TAA AGG GTG GTA GGC ATC TCA TCT TCT GCC ATT 334  
Phe Pro Leu Leu Leu \* Arg Val Val Gly Ile Ser Ser Ser Ala Ile  
100 105 110

CCA AGA AAA AAT GTG ATG AAC TCG CCA AGC AAC TGA CCA GCC TGG GCG 382  
Pro Arg Lys Asn Val Met Asn Ser Pro Ser Asn \* Pro Ala Trp Ala  
115 120 125

TGA ACG CCG TGG CAT ATT ATA GAG GTC TAG ACG TCG CCG TCA TAC CCA 430  
\* Thr Pro Trp His Ile Ile Glu Val \* Thr Ser Pro Ser Tyr Pro  
130 135 140

CAA CAG GAG ACG TGG TCG TGT GCA GCA CCG ACG CGC TCA TGA CGG GAT 478  
Gln Gln Glu Thr Trp Ser Cys Ala Ala Pro Thr Arg Ser \* Arg Asp  
145 150 155

TCA CCG GCG ACT TTG ATT CTG TCA TAG ACT GCA ACT CCG CCG TCA CTC 526  
Ser Pro Ala Thr Leu Ile Leu Ser \* Thr Ala Thr Pro Pro Ser Leu  
160 165 170 175

AGA CGG TGG ACT TCA GTC TGG ATC CCA CTT TTA CCA TTG AGA CTA CCA 574  
Arg Arg Trp Thr Ser Val Trp Ile Pro Leu Leu Pro Leu Arg Leu Pro  
180 185 190

CAG TGC CCC AGG ACG CAG TGT CCA GAA GCC AGC GTT GGG GCC GCA CGG 622  
Gln Cys Pro Arg Thr Gln Cys Pro Glu Ala Ser Val Gly Ala Ala Arg  
195 200 205

GGA GAG GTA GGC ACG GCA TAT ACC GGT ATG TCT CGG CTG GAG AGA GAC 670  
Gly Glu Val Gly Thr Ala Tyr Thr Gly Met Ser Arg Leu Glu Arg Asp  
210 215 220

CGT CTG GCA TGT TCG ACT CCG TGG TGC TCT GTG AGT GCT ACG ATG CCG 718  
Arg Leu Ala Cys Ser Thr Pro Trp Cys Ser Val Ser Ala Thr Met Pro

[illegible]



225	230	235	
GAT GTG CAT GGT ACG ATC TGA CTC CTG CCG AGA CTA CCG TGA GGT TGC Asp Val His Gly Thr Ile * Leu Leu Pro Arg Leu Pro * Gly Cys 240 245 250 255			
GCG CTT ACT AAA CAC CCC CGG GCT CCC TGT CTG TCA GGA CCA TTT GGA Ala Leu Thr Lys His Pro Arg Ala Pro Cys Leu Ser Gly Pro Phe Gly 260 265 270			
ATT CTG GGA GGG GGT GTT CAC GGG GCT CAC TAA CAT CGA CGC TCA CAT Ile Leu Gly Gly Gly Val His Gly Ala His * His Arg Arg Ser His 275 280 285			86
GCT GTC ACA GAC CAA ACA GGG TGG GGA GAA TTT CCC ATA CCT TGT AGC Ala Val Thr Asp Gln Thr Gly Trp Gly Glu Phe Pro Ile Pro Cys Ser 290 295 300			910
GTA CCA AGC AAC AGT CTG TGT TCG CGC GAA AGC GCC CCC CCC CAG CTG Val Pro Ser Asn Ser Leu Cys Ser Arg Glu Ser Ala Pro Pro Gln Leu 305 310 315			958
GGA CAC AAT GTG GAA ATG CAT GCT CCG TCT CAA ACC GAC TTA ACT GGC Gly His Asn Val Glu Met His Ala Pro Ser Gln Thr Asp Leu Thr Gly 320 325 330 335			1006
CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC ACA Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile Thr 340 345 350			1054
CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG GAC Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp 355 360 365			1102
TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG GCG Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val Ala 370 375 380			1150
GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC GGT Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val Gly 385 390 395			1198
AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG GTA Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu Val 400 405 410 415			1246
TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG CCC Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu Pro 420 425 430			1294
TAT ATG GAC GAA ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA GTG Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys Val 435 440 445			1342
CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG CCG Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys Pro 450 455 460			1390

GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG CCA CAT ACA 1438  
 Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Pro His Thr  
 465 470 475

TGT GGA ACT TCA TCA GTG GGA TAC AAT AAT AG 1470  
 Cys Gly Thr Ser Ser Val Gly Tyr Asn Asn  
 480 485

## (2) INFORMATION FOR SEQ ID NO: 197:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TGTGCCAGGA CCATCACCAC CGGAGCTTCT ATCACATACT CCACTTACGG CAAGTTCCTT 60  
 GCTGATGGAG GGTGTTTCAGG CGGCGCGCAT GACGTGATCA TATGCGACGA GTGCCATTCC 120  
 CAGGACGCCA CCACCATTTCT TGGGATAGGC ACTGTCCTTG ACCAGGCAGA GACGGCTGGA 180  
 GCTAGGCTCG TCGTCTTGGC CACGGCCACC CCTCCCGGCA GTGTGACAAC GCCCCACCCC 240  
 AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTT CTTTCTACGG CAGAGCCATT 300  
 CCCCTTGCTT TTATAAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAATGT 360  
 GATGAACCTG CCAAGCAACT GACCAGCCTG GCGTGAACG CCGTGGCATA TTATAGAGGT 420  
 CTAGACGTCG CCGTCATACC CACAACAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC 480  
 ATGACGGGAT TCACCGGCGA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG 540  
 ACGGTGGACT TCAGTCTGGA TCCCACCTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC 600  
 GCAGTGTCCA GAAGCCAGCG TTGGGGCCGC ACGGGGAGAG GTAGGCACGG CATATACCGG 660  
 TATGTCTCGG CTGGAGAGAG ACCGTCTGGC ATGTTGACT CCGTGGTGCT CTGTGAGTGC 720  
 TACGATGCCG GATGTGCATG GTACGATCTG ACTCCTGCCG AGACTACCGT GAGGTTGCGC 780  
 GCTTACNTAA ACACCCCCGG GCTCCCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG 840  
 GTGTTACCGG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG 900  
 GAGAATTTCC CATACCTTGT AGCGTACCAA GCAACAGTCT GTGTTGCGGC GAAAGCGCCC 960

CCCCCCAGCT GGGACACAAT GTGGAAATGC ATGCTCCGTC TCAAACCGAC NTTAACTGGC 1020  
 CCTACTCCCC TCTGTACAG GCTGGGGCCC GTCCAGAATG AGATCACACT GACGCACCCC 1080  
 ATCACCAGT ACATTATGGC TTGCATGTCT GCGGACTTGG AGGTCATTAC CAGCACTTGG 1140  
 GTTCTGGTGG GGGGCGTTGT GGGGGCCCTG GCGGCCTACT GCTTGACGGT GGGTTCGGTA 1200  
 GCCATAGTCG GTAGGATCAT CCTCTCTGGG AAACCTGCCA TCATTCCCGA TAGGGAGGTA 1260  
 TTATACCAGC AATTGATGA GATGGAGGAG TGCTCGGCCT CGTTGCCCTA TATGGACGAA 1320  
 ACACGTGCCA TTGCCGGACA ATTCAAAGAG AAAGTGCTCG GCTTCATCAG CACGACCGGC 1380  
 CAGAAGGCTG AAACCTCTGAA GCCGGCAGCC ACGTCTGTGT GGAACAAGGC TGAGCAGTTC 1440  
 TGGNCCACAT ACATGTGGAA CTTCAATCAGT GGGATACAAT AATAG 1485

## (2) INFORMATION FOR SEQ ID NO: 198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 484 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Cys	Ala	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Ser	Ile	Thr	Tyr	Ser	Thr	Tyr
1					5				10					15	
Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	His	Asp	Val
			20					25					30		
Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Gln	Asp	Ala	Thr	Thr	Ile	Leu	Gly
			35				40						45		
Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val
			50			55					60				
Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Thr	Pro	His	Pro
			65			70				75				80	
Asn	Ile	Glu	Glu	Val	Ala	Leu	Pro	Gln	Glu	Gly	Glu	Val	Pro	Phe	Tyr
			85					90						95	
Gly	Arg	Ala	Ile	Pro	Leu	Ala	Phe	Ile	Lys	Gly	Gly	Arg	His	Leu	Ile
			100					105					110		
Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Lys	Gln	Leu	Thr
			115				120					125			
Ser	Leu	Gly	Val	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ala
			130			135						140			

Val Ile Pro Thr Thr Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu  
 145 150 155 160  
 Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser  
 165 170 175  
 Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile  
 180 185 190  
 Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Trp  
 195 200 205  
 Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala  
 210 215 220  
 Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Val Val Leu Cys Glu Cys  
 225 230 235 240  
 Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr  
 245 250 255  
 Val Arg Leu Arg Ala Tyr Xaa Asn Thr Pro Gly Leu Pro Val Cys Gln  
 260 265 270  
 Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile  
 275 280 285  
 Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro  
 290 295 300  
 Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro  
 305 310 315 320  
 Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro  
 325 330 335  
 Xaa Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln  
 340 345 350  
 Asn Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys  
 355 360 365  
 Met Ser Ala Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly  
 370 375 380  
 Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val  
 385 390 395 400  
 Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro  
 405 410 415  
 Asp Arg Glu Val Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser  
 420 425 430  
 Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe  
 435 440 445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu  
450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe  
465 470 475 480

Trp Xaa Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TGTGCCAGGA CCATCACCAC CGGAGCTTCT ATCACA TACT CCAC TTACGG CAAGTTCCTT	60
GCTGATGGAG GGTGTT CAGG CGGCGCGTAT GACGTGATCA TATGCGACGA GTGCCATTCC	120
CAGGACGCCA CCACCATTCT TGGGATAGGC ACTGTCCTTG ACCAGGCAGA GACGGCTGGA	180
GCTAGGCTCG TCGTCTTGGC CACGGCCACC CCTCCCGGCA GTGTGACAAC GCCCCACCCC	240
AACATCGAGG AAGTGGCCCT GCCTCAGGAG GGGGAGGTTC CCTTCTACGG CAGAGCCATT	300
CCCCTTGCTT TTATAAGGG TGGTAGGCAT CTCATCTTCT GCCATTCCAA GAAAAAATGT	360
GATGAAC TCG CCAAGCAACT GACCAGCCTG GCGGTGAACG CCGTGGCATA TTATAGAGGT	420
CTAGACGTCG CCGTCATCCC CACAGCAGGA GACGTGGTCG TGTGCAGCAC CGACGCGCTC	480
ATGACGGGAT TCACCGGGCA CTTTGATTCT GTCATAGACT GCAACTCCGC CGTCACTCAG	540
ACGGTGGACT TCAGTCTGGA TCCCACTTTT ACCATTGAGA CTACCACAGT GCCCCAGGAC	600
GCAGTGTCCA GAAGCCAGCG TAGGGGCGCG ACGGGGAGAG GTAGGCACGG CATATACCGG	660
TATGTCTCGG CTGGAGAGAG ACCNTCTGAC ATGTTGCGACT CCGTGGTGCT CTGTGAGTGC	720
TACGATGCCG GATGTGCGTG GTATGATCTG ACTCCTGCCG AGACTACCGT GAGGTTGCCG	780
GCTTACATAA ACACCCCCGG GCTCCCTGTC TGTCAGGACC ATTTGGAATT CTGGGAGGGG	840
GTGTTACACG GGCTCACTAA CATCGACGCT CACATGCTGT CACAGACCAA ACAGGGTGGG	900
GAGAATTTNC CATACTTGT AGCGTACCAA GCAACAGTCT GTGTTGCGCG GAAAGCGCCC	960

```

CCCCCCAGCT GGGACACAAT GTGGAAATGC ATGCTCCGTC TCAAACCGAC TTAACTGGC 0
CCTACTCCCC TCTTGACAG GCTGGGGCCC GTCCAGANTG AGATCACACT GACGCACCCC 3
ATCACCAAGT ACATTATGGC TTGCATGTCT GCGGACTTGG AGGTCATTAC CANCACTTGG 10
GTTCTGGTGG GGGGCGTTGT GCGGGCCCTG GCGGCCTACT GCTTGACGGT GGGTTCGGTA 126
GCCATAGTCG GTAGGATCAT CCTCTCTGGG AAACCTGCCA TCATTCCCGA TAGGGAGGCA 1260
TTATACCAGC AATTGTATGA GATGGAGGAG TGCTCGGCCT CGTTGCCCTA TATGGACGAG 1320
ACACGTGCCA TTGCCGGACA ATTCAAAGAG AAAGTGCTCG GCTTCATCAG CACGACCGGC 1380
CAGAAGGCTG AAACCTCTGAA GCGGGCAGCC ACGTCTGTGT GGAACAAGGC TGAGCAGTTC 1440
TGGGCCACAT ACATGTGGAA CTTTCATCAGC GGGATACAAT AATAG 1485

```

## (2) INFORMATION FOR SEQ ID NO: 200:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

Cys Ala Arg Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr
1           5           10           15
Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val
20          25          30
Ile Ile Cys Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly
35          40          45
Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val
50          55          60
Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro
65          70          75          80
Asn Ile Glu Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr
85          90          95
Gly Arg Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile
100         105         110
Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr
115         120         125

```

Ser Leu Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala  
 130 135 140  
 Val Ile Pro Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu  
 145 150 155 160  
 Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser  
 165 170 175  
 Ala Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile  
 180 185 190  
 Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg  
 195 200 205  
 Gly Arg Thr Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala  
 210 215 220  
 Gly Glu Arg Xaa Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys  
 225 230 235 240  
 Tyr Asp Ala Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr  
 245 250 255  
 Val Arg Leu Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln  
 260 265 270  
 Asp His Leu Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile  
 275 280 285  
 Asp Ala His Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Xaa Pro  
 290 295 300  
 Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro  
 305 310 315 320  
 Pro Pro Ser Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro  
 325 330 335  
 Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln  
 340 345 350  
 Xaa Glu Ile Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys  
 355 360 365  
 Met Ser Ala Asp Leu Glu Val Ile Thr Xaa Thr Trp Val Leu Val Gly  
 370 375 380  
 Gly Val Val Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val  
 385 390 395 400  
 Ala Ile Val Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro  
 405 410 415  
 Asp Arg Glu Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser  
 420 425 430  
 Ala Ser Leu Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe

09073224 060504

435

440

445

Lys Glu Lys Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu  
 450 455 460

Thr Leu Lys Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe  
 465 470 475 480

Trp Ala Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

C	TCC	ACT	GTG	ACT	GAG	AGA	GAC	ATC	AGG	GTC	GAA	GAA	GAA	GTC	TAT	46	
	Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Val	Glu	Glu	Glu	Val	Tyr		
	1				5					10					15		
	CAG	TGT	TGT	GAT	CTG	GAG	CCC	GAG	GCC	CGC	AAG	GTA	ATA	ACC	GCC	CTC	94
	Gln	Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Thr	Ala	Leu	
					20					25					30		
	ACG	GAG	AGA	CTC	TAC	GTG	GGC	GGC	CCT	ATG	TAC	AAT	AGC	AAG	GGA	GAC	142
	Thr	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Tyr	Asn	Ser	Lys	Gly	Asp	
					35					40					45		
	CTT	TGC	GGG	TAT	CGC	AGG	TGC	CGC	GCA	AGC	GGC	GTA	TAT	ACC	ACC	AGC	190
	Leu	Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr	Ser	
					50				55						60		
	TTC	GGG	AAC	ACA	CTG	ACG	TGC	TAC	CTT	AAA	GCC	TCA	GCA	GCC	ATC	AGG	238
	Phe	Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Ser	Ala	Ala	Ile	Arg	
					65				70						75		
	GCT	GCG	GGG	CTG	AAG	GAC	TGC	ACC	ATG	CTG	GTT	TGC	GGT	GAC	GAC	TTA	286
	Ala	Ala	Gly	Leu	Lys	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	
					80				85						90		95



GTC GTG ATC GCT GAA AGC GGT GGC GTC GAG GAG GAC AAG CGA GCC CTC 334  
 Val Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu  
                     100                    105                    110

GGA GCT 340  
 Gly Ala

## (2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln  
       1                    5                    10                    15  
 Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr  
                     20                    25                    30

Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu  
                     35                    40                    45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
                     50                    55                    60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala  
                     65                    70                    75                    80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
                     85                    90                    95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Lys Arg Ala Leu Gly  
                     100                    105                    110

Ala

## (2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 2..340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 2..337

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

C TCC ACA GTG ACT GAA AGA GAC ATC AGG GTC GAG GAA GAG GTC TAC	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr	
1 5 10 15	
CAG TGT TGT GAC CTG GAG CCT GAA ACC CGC AAG GTA ATA TCT GCC CTC	94
Gln Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu	
20 25 30	
ACT GAA AGA CTC TAT GTG GGC GGT CCC ATG CAC AAC AGC AGG GGA GAC	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp	
35 40 45	
CTA TGC GGG TAC CGT AGA TGC CGC GCG AGC GGC GTA TAC ACC ACA AGC	190
Leu Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACT CTG ACG TGC TTC CTC AAG GCC ACA GCG GCC ACC AAA	238
Phe Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys	
65 70 75	
GCC GCT GGC CTA AAG GAC TGC ACC ATG TTG GTG TGT GGT GAC GAC TTA	286
Ala Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTT ATC GCC GAA AGC GAT GGT GTC GAA GAG GAC CGC CGA GCC CTC	334
Val Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu	
100 105 110	
GGA GCT	340
Gly Ala	

## (2) INFORMATION FOR SEQ ID NO: 204:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln
1 5 10 15

Cys Cys Asp Leu Glu Pro Glu Thr Arg Lys Val Ile Ser Ala Leu Thr  
20 25 30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Arg Gly Asp Leu  
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
50 55 60

Gly Asn Thr Leu Thr Cys Phe Leu Lys Ala Thr Ala Ala Thr Lys Ala  
65 70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Arg Arg Ala Leu Gly  
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

C TCC ACG GTG ACC GAA AGG GAT ATC AGG ACC GAG GAA GAG ATC TAC 46  
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr  
1 5 10 15

CAG TGC TGC GAC CTG GAG CCC GAA GCC CGC AAG GTG ATA TCC GCC CTA 94  
Gln Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu  
20 25 30

ACG GAA AGA CTC TAC GTG GGC GGT CCC ATG TAC AAC TCC AAG GGG GAC 142  
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp  
35 40 45

CTA TGC GGG CAA CGG AGG TGC CGC GCA AGC GGG GTC TAC ACC ACC AGC	190
Leu Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser	
50 55 60	
TTC GGG AAC ACT GTA ACG TGT TAT CTC AAG GCC GTT GCG GCT ACT AGG	238
Phe Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg	
65 70 75	
GCC GCA GGT CTG AAA GGT TGC AGC ATG CTG GTT TGT GGA GAC GAC TTA	286
Ala Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATC TGC GAG AGC GGC GGC GTA GAG GAG GAT GCA AGA GCC CTC	334
Val Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu	
100 105 110	
CGA GCC	340
Arg Ala	

## (2) INFORMATION FOR SEQ ID NO: 206:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Glu Ile Tyr Gln	
1 5 10 15	
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr	
20 25 30	
Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu	
35 40 45	
Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe	
50 55 60	
Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Val Ala Ala Thr Arg Ala	
65 70 75 80	
Ala Gly Leu Lys Gly Cys Ser Met Leu Val Cys Gly Asp Asp Leu Val	
85 90 95	
Val Ile Cys Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg	
100 105 110	
Ala	

## (2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 2..340

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 2..337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

C	TCC	ACG	GTG	ACT	GAA	AGG	GAC	ATT	AGG	GTC	GAG	GAA	GAG	ATC	TAC	46	
	Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Val	Glu	Glu	Glu	Ile	Tyr		
	1				5					10					15		
	CAG	TGC	TGT	GAC	CTG	GAG	CCC	GAG	GCA	CGC	AAG	GTG	ATA	TCC	GCT	CTC	94
	Gln	Cys	Cys	Asp	Leu	Glu	Pro	Glu	Ala	Arg	Lys	Val	Ile	Ser	Ala	Leu	
				20						25					30		
	ACA	GAA	AGA	CTC	TAC	AAG	GGC	GGC	CCC	ATG	TAT	AAC	AGC	AAG	GGG	GAC	142
	Thr	Glu	Arg	Leu	Tyr	Lys	Gly	Gly	Pro	Met	Tyr	Asn	Ser	Lys	Gly	Asp	
				35					40					45			
	CTA	TGC	GGG	CTT	CGG	AGG	TGC	CGC	GCA	AGC	GGG	GTA	TAC	ACC	ACA	AGC	190
	Leu	Cys	Gly	Leu	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Tyr	Thr	Thr	Ser	
				50				55					60				
	TTC	GGG	AAC	ACG	GTG	ACA	TGC	TAC	CTT	AAA	GCC	ACA	GCA	GCC	ACC	AGG	238
	Phe	Gly	Asn	Thr	Val	Thr	Cys	Tyr	Leu	Lys	Ala	Thr	Ala	Ala	Thr	Arg	
				65				70					75				
	GCT	GCA	GGG	CTG	AAA	GAT	TGC	ACT	ATG	CTG	GTA	TGC	GGT	GAC	GAC	TTA	286
	Ala	Ala	Gly	Leu	Lys	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	
				80			85				90				95		
	GTC	GTT	ATT	GCC	GAA	AGC	GGT	GGC	GTG	GAG	GAG	GAC	GCC	CGA	GCC	CTC	334
	Val	Val	Ile	Ala	Glu	Ser	Gly	Gly	Val	Glu	Glu	Asp	Ala	Arg	Ala	Leu	
				100					105				110				
	CGA	GCC															340
	Arg	Ala															

(2) INFORMATION FOR SEQ ID NO: 208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
 1             5             10             15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ala Leu Thr
          20             25             30

Glu Arg Leu Tyr Lys Gly Gly Pro Met Tyr Asn Ser Lys Gly Asp Leu
          35             40             45

Cys Gly Leu Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
          50             55             60

Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
          65             70             75             80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
          85             90             95

Val Ile Ala Glu Ser Gly Gly Val Glu Glu Asp Ala Arg Ala Leu Arg
          100            105            110

Ala
  
```

## (2) INFORMATION FOR SEQ ID NO: 209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..340

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

CCCCACCGTG ACNGAGAGGG ACNTCAGGGT CGAGGAAGAG GTCTATCAGT GCTGTAATCT      60
GGAGNCCGAT GNCCGCAAGG TCATCAACGC CCTCACAGAG AGACTCTACG TGGGCGGCC      120
  
```

TATGCACAAC AGCAAGGGAG ACCTGTGTGG CATCCGTAGA TGCCGCGCGA GCGGCGTTTA 180  
 CACCACGAGC TTCGGAAACA CGCTGACTTG CTACCTCAA GCCACAGCGG CCACCAGGGC 240  
 CGCGGGCTTG AAGGATTGCA CCATGCTGGT CTGCGGAGAC GACCTGGTTG TCATTGCTGA 300  
 GAGCATTGGC ATAGACGAGG ACAAGCAAGC COTCCGACT 340

## (2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

Pro Thr Val Thr Glu Arg Asp Xaa Arg Val Glu Glu Glu Val Tyr Gln  
 1 5 10 15  
 Cys Cys Asn Leu Glu Xaa Asp Xaa Arg Lys Val Ile Asn Ala Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu  
 35 40 45  
 Cys Gly Ile Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe  
 50 55 60  
 Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala  
 65 70 75 80  
 Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ala Glu Ser Ile Gly Ile Asp Glu Asp Lys Gln Ala Leu Arg  
 100 105 110  
 Thr

## (2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```

CTCGACTGTG NCCGAGAGGG ACATCAGGAC AGAGGGAGAG GTCTATCAGT GTTGCGACCT      60
GGAACCGGAA GCCCGCAAGG TAATCACCGC CCTCACTGAG AGACTCTATG TGGGCGGACC      120
CATGTTCAAC AGCAAGGGAG ACCTGTGCGG ACAACGCCGG TGCCGCGCAA GCGGCGTGTT      180
CACCACCAGC TTCGGGAACA CACTGACGTG CTACCTTAAA GCCACAGCTG CTACTAGAGC      240
AGCCGGCTTA AAAGATTGCA CCATGCTGGT CTGCGGTGAC GACTTAGTCG TTATTTCGGA      300
GAGCGCCGGT GTGGAGGAGG ATCCCANAA CCGGCGACCN                               340
  
```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```

Ser Thr Val Xaa Glu Arg Asp Ile Arg Thr Glu Gly Glu Val Tyr Gln
1           5           10           15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
20           25           30
Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu
35           40           45
Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Phe
50           55           60
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala
  
```



65

70

75

80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95

Val Ile Ser Glu Ser Ala Gly Val Glu Glu Asp Pro Xaa Thr Xaa Arg  
100 105 110

Pro

## (2) INFORMATION FOR SEQ ID NO: 213:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..337

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

C TCA ACA GTC ACC GAG AAC GAC ATC CGT GTT GAG GAG TCA ATT TAC	46
Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr	
1 5 10 15	
CAA TGT TGT GAC TTG GCC CCC GAG GCC AGA CAG GCC ATA AAG TCG CTC	94
Gln Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu	
20 25 30	
ACA GAG CGG CTT TAT ATC GGG GGT CCC CTG ACT AAT TCA AAG GGG CAG	142
Thr Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln	
35 40 45	
AAC TGT GGC TAT CGC CGA TGC CGC GCA AGC GGC GTG CTG ACG ACC AGC	190
Asn Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser	
50 55 60	
TGC GGT AAT ACC CTT ACA TGT TAC CTA AAG GCC TCT GCA GCC TGT CGA	238
Cys Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg	
65 70 75	
GCT GCG AAG CTC CAG GAC TGC ACG ATG CTC GTG TGC GGG GAC GAC CTT	286

Ala Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu  
 80 85 90 95

GTC GTT ATC TGT GAA AGC GCG GGA ACC CAA GAG GAC GCG GCG AGC CTA 334  
 Val Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu  
 100 105 110

CGA GTC 340  
 Arg Val

## (2) INFORMATION FOR SEQ ID NO: 214:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln  
 1 5 10 15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Gln Ala Ile Lys Ser Leu Thr  
 20 25 30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn  
 35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys  
 50 55 60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Cys Arg Ala  
 65 70 75 80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95

Val Ile Cys Glu Ser Ala Gly Thr Gln Glu Asp Ala Ala Ser Leu Arg  
 100 105 110

Val

## (2) INFORMATION FOR SEQ ID NO: 215:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..340

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 2..340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

C TCA ACC GTC ACG GAG AGG GAT ATA AGA ACA GAA GAA TCC ATA TAT	46
Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr	
1 5 10 15	
CAA GCT TGT TCC CTG CCC CAA GAG GCC AGA ACT GTC ATA CAC TCG CTC	94
Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu	
20 25 30	
ACC GAG AGA CTC TAC GTG GGA GGG CCC ATG ATA AAC AGC AAA GGG CAA	142
Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln	
35 40 45	
TCC TGC GGT TAC AGG CGT TGC CGC GCA AGC GGT GTT TTC ACC ACC AGC	190
Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser	
50 55 60	
ATG GGG AAT ACC ATG ACG TGT TAC ATC AAA GCC CTT GCA GCG TGT AAA	238
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys	
65 70 75	
GCC GCA GGG ATC GTG GAC CCC GTC ATG CTG GTG TGT GGA GAC GAC CTG	286
Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu	
80 85 90 95	
GTC GTC ATC TCG GAG AGC CAG GGT AAC GAG GAG GAC GAG CGA AAC CTG	334
Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu	
100 105 110	
AGA GCT	340
Arg Ala	

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln  
 1 5 10 15  
 Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met Ile Asn Ser Lys Gly Gln Ser  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met  
 50 55 60  
 Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala  
 65 70 75 80  
 Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu Arg  
 100 105 110  
 Ala

## (2) INFORMATION FOR SEQ ID NO: 217:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..340

## (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 2..340

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

C TCG ACT GTC ACT GAA CAG GAC ATC AGG GTG GAA GAG GAG ATA TAT  
 Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr  
 1 5 10 15  
 CAA TGC TGC AAC CTT GAA CCG GAG GCC AGG AAA GTG ATC TCC TCC CTC  
 Gln Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu  
 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 94

20	25	30	
ACG GAG CGG CTT TAC TGC GGA GGC CCT ATG TTT AAC AGC AAG GGG GCC			142
Thr Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala			
35	40	45	
CAG TGT GGT TAT CGC CGT TGC CGT GCC AGT GGA GTT CTG CCT ACC AGC			190
Gln Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser			
50	55	60	
TTT GGC AAC ACA ATC ACT TGT TAC ATC AAG GCC ACA ACG GCC GCG AAG			238
Phe Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys			
65	70	75	
GCC GCA GGC CTC CGG AAC CCG GAC TTT CTT GTC TGC GGA GAT GAT CTG			286
Ala Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu			
80	85	90	95
GTC GTG GTG GCT GAG AGT GAT GGC GTC GAC GAG GAT AGA GCA GCC CTG			334
Val Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu			
100	105	110	
AGA GCC			340
Arg Ala			

## (2) INFORMATION FOR SEQ ID NO: 218:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln			
1	5	10	15
Cys Cys Asn Leu Glu Pro Glu Ala Arg Lys Val Ile Ser Ser Leu Thr			
20	25	30	
Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Ala Gln			
35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe			
50	55	60	
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Thr Thr Ala Ala Lys Ala			
65	70	75	80
Ala Gly Leu Arg Asn Pro Asp Phe Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	
Val Val Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Ala Ala Leu Arg			
100	105	110	

Ala

## (2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

Arg	Ser	Glu	Gly	Arg	Thr	Ser	Trp	Ala	Gln
1				5				10	

## (2) INFORMATION FOR SEQ ID NO: 220:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

Arg	Ser	Glu	Gly	Arg	Thr	Ser	Trp	Ala	Gln
1				5				10	

## (2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

Arg	Thr	Glu	Gly	Arg	Thr	Ser	Trp	Ala	Gln
1				5				10	

## (2) INFORMATION FOR SEQ ID NO: 222:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 629 base pairs

- (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 3..629

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 3..629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

TA GAC TTT TGG GAG AGC GTC TTC ACT GGA CTA ACT CAC ATA GAT GCC	47
Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala	
1 5 10 15	
CAC TTT CTG TCA CAG ACT AAG CAG CAG GGA CTC AAC TTC TCG TTC CTG	95
His Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu	
20 25 30	
ACT GCC TAC CAA GCC ACT GTG TGC GCT CGC GCG CAG GCT CCT CCC CCA	143
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro	
35 40 45	
AGT TGG GAC GAG ATG TGG AAG TGT CTC GTA CGG CTT AAG CCA ACA CTA	191
Ser Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu	
50 55 60	
CAT GGA CCT ACG CCT CTT CTA TAT CGG TTG GGG CCT GTC CAA AAT GAA	239
His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu	
65 70 75	
ATC TGC TTG ACA CAC CCC ATC ACA AAA TAC ATC ATG GCA TGC ATG TCA	287
Ile Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser	
80 85 90 95	
GCT GAT CTG GAA GTA ACC ACC AGC ACC TGG GTT TTG CTT GGA GGG GTC	335
Ala Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val	
100 105 110	
CTC GCG GCC CTA GCG GCC TAC TGC TTG TCA GTC GGT TGT GTT GTG ATT	383
Leu Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile	
115 120 125	
GTG GGT CAT ATC GAG CTG GGG GGC AAG CCG GCA ATC GTT CCA GAC AAA	431
Val Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys	
130 135 140	

00983224 060501

GAG GTG TTG TAT CAA CAA TAC GAT GAG ATG GAA GAG TGC TCA CAA GCT	479
Glu Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala	
145 150 155	
GCC CCA TAT ATC GAA CAA GCT CAG GTA ATA GCT CAC CAG TTC AAG GAA	527
Ala Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu	
160 165 170 175	
AAA GTC CTT GGA TTG CTG CAG CGA GCC ACC CAA CAA CAA GCT GTC ATT	575
Lys Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile	
180 185 190	
GAG CCC ATA GTA ACT ACC AAC TGG CAA AAG CTT GAG GCC TTT TGG CAC	623
Glu Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His	
195 200 205	
AAG CAT	629
Lys His	

## (2) INFORMATION FOR SEQ ID NO: 223:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

Asp Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His	
1 5 10 15	
Phe Leu Ser Gln Thr Lys Gln Gln Gly Leu Asn Phe Ser Phe Leu Thr	
20 25 30	
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser	
35 40 45	
Trp Asp Glu Met Trp Lys Cys Leu Val Arg Leu Lys Pro Thr Leu His	
50 55 60	
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile	
65 70 75 80	
Cys Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	
85 90 95	
Asp Leu Glu Val Thr Thr Ser Thr Trp Val Leu Leu Gly Gly Val Leu	
100 105 110	
Ala Ala Leu Ala Ala Tyr Cys Leu Ser Val Gly Cys Val Val Ile Val	
115 120 125	
Gly His Ile Glu Leu Gly Gly Lys Pro Ala Ile Val Pro Asp Lys Glu	
130 135 140	

T05090"422E2860



Val Leu Tyr Gln Gln Tyr Asp Glu Met Glu Glu Cys Ser Gln Ala Ala  
 145 150 155 160

Pro Tyr Ile Glu Gln Ala Gln Val Ile Ala His Gln Phe Lys Glu Lys  
 165 170 175

Val Leu Gly Leu Leu Gln Arg Ala Thr Gln Gln Gln Ala Val Ile Glu  
 180 185 190

Pro Ile Val Thr Thr Asn Trp Gln Lys Leu Glu Ala Phe Trp His Lys  
 195 200 205

His

(2) INFORMATION FOR SEQ ID NO: 224:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 2..12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

Ile His Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

Val Asn Tyr Arg Asn Ala Ser Gly Ile Tyr His Ile  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:

09873224.060501

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

Val Asn Tyr His Asn Thr Ser Gly Ile Tyr His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

Gln His Tyr Arg Asn Ala Ser Gly Ile Tyr His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

Ile His Tyr Arg Asn Ala Ser Asp Gly Tyr Tyr Ile  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

Leu Gln Val Lys Asn Thr Ser Ser Ser Tyr Met Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

Val Trp Gln Leu Arg Ala Ile Val Leu His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

Val	Tyr	Glu	Ala	Asp	Tyr	His	Ile	Leu	His	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Val	Tyr	Glu	Thr	Asp	Asn	His	Ile	Leu	His	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

Val	Tyr	Glu	Thr	Glu	Asn	His	Ile	Leu	His	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 236:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

Val Phe Glu Thr Val His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

Val Phe Glu Thr Glu His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

Val Phe Glu Thr Asp His His Ile Met His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

Val Tyr Glu Thr Glu Asn His Ile Leu His Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 240:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 11 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

Val Tyr Glu Ala Asp Ala Leu Ile Leu His Ala  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 241:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

Val Gln Asp Gly Asn Thr Ser Ala Cys Trp Thr Pro Val  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Val Arg Thr Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

Val Lys Thr Gly Asn Gln Ser Arg Cys Trp Ile Ala Leu

1

5

10

## (2) INFORMATION FOR SEQ ID NO: 247:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

Val Lys Thr Gly Asn Ser Val Arg Cys Trp Ile Pro Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 248:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

Val Lys Thr Gly Asn Val Ser Arg Cys Trp Ile Ser Leu  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 249:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

Val Arg Lys Asp Asn Val Ser Arg Cys Trp Val Gln Ile  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 250:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid



- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

Ala Pro Ser Phe Gly Ala Val Thr Ala Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

Val Ser Gln Pro Gly Ala Leu Thr Lys Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

Val Lys Tyr Val Gly Ala Thr Thr Ala Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

Ala Pro Tyr Ile Gly Ala Pro Val Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

Ala Gln His Leu Asn Ala Pro Leu Glu Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

Ser Pro Tyr Val Gly Ala Pro Leu Glu Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 256:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

Ser Pro Tyr Ala Gly Ala Pro Leu Glu Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

Ala	Pro	Tyr	Leu	Gly	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

Ala	Pro	Tyr	Leu	Gly	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 259:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

Ala	Pro	Tyr	Val	Gly	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 260:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

Asn Val Pro Tyr Leu Gly Ala Pro Leu Thr Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

Ala Pro His Leu Arg Ala Pro Leu Ser Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

Ala Pro Tyr Leu Gly Ala Pro Leu Thr Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

Arg Pro Arg Gln His Ala Thr Val Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 264:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

Ser	Pro	Gln	His	His	Lys	Phe	Val	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 265:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

Arg	Pro	Arg	Arg	Leu	Trp	Thr	Thr	Gln	Glu
1				5					10

(2) INFORMATION FOR SEQ ID NO: 266:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

Pro	Pro	Arg	Ile	His	Glu	Thr	Thr	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

Thr Ile Ser Tyr Ala Asn Gly Ser Gly Pro Ser Asp Asp Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

Ser Arg Arg Gln Pro Ile Pro Arg Ala Arg Arg Thr Glu Gly Arg Ser  
1 5 10 15  
Trp Ala Gln

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1443 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..1443

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide  
(B) LOCATION: 1..1443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ACC ATC ACC ACC GGA GCT TCT ATC ACA TAC TCC ACT TAC GGC AAG TTC  
Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe

48

1	5	10	15	
CTT GCT GAT GGA GGG TGT TCA GGC GGC GCG TAT GAC GTG ATC ATA TGC				96
Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys				
20	25	30		
GAC GAG TGC CAT TCC CAG GAC GCC ACC ACC ATT CTT GGG ATA GGC ACT				144
Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr				
35	40	45		
GTC CTT GAC CAG GCA GAG ACG GCT GGA GCT AGG CTC GTC GTC TTG GCC				192
Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala				
50	55	60		
ACG GCC ACC CCT CCC GGC AGT GTG ACA ACG CCC CAC CCC AAC ATC GAG				240
Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu				
65	70	75	80	
GAA GTG GCC CTG CCT CAG GAG GGG GAG GTT CCC TTC TAC GGC AGA GCC				288
Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala				
85	90	95		
ATT CCC CTT GCT TTT ATA AAG GGT GGT AGG CAT CTC ATC TTC TGC CAT				336
Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His				
100	105	110		
TCC AAG AAA AAA TGT GAT GAA CTC GCC AAG CAA CTG ACC AGC CTG GGC				384
Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly				
115	120	125		
GTG AAC GCC GTG GCA TAT TAT AGA GGT CTA GAC GTC GCC GTC ATC CCC				432
Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro				
130	135	140		
ACA GCA GGA GAC GTG GTC GTG TGC AGC ACC GAC GCG CTC ATG ACG GGA				480
Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly				
145	150	155	160	
TTC ACC GGC GAC TTT GAT TCT GTC ATA GAC TGC AAC TCC GCC GTC ACT				528
Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr				
165	170	175		
CAG ACG GTG GAC TTC AGT CTG GAT CCC ACT TTT ACC ATT GAG ACT ACC				576
Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr				
180	185	190		
ACA GTG CCC CAG GAC GCA GTG TCC AGA AGC CAG CGT AGG GGC CGC ACG				624
Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr				
195	200	205		
GGG AGA GGT AGG CAC GGC ATA TAC CGG TAT GTC TCG GCT GGA GAG AGA				672
Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg				
210	215	220		
CCG TCT GAC ATG TTC GAC TCC GTG GTG CTC TGT GAG TGC TAC GAT GCC				720
Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala				
225	230	235	240	

GGA TGT GCG TGG TAT GAT CTG ACT CCT GCC GAG ACT ACC GTG AGG TTG	768
Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu	
245 250 255	
CGC GCT TAC ATA AAC ACC CCC GGG CTC CCT GTC TGT CAG GAC CAT TTG	816
Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu	
260 265 270	
GAA TTC TGG GAG GGG GTG TTC ACG GGG CTC ACT AAC ATC GAC GCT CAC	864
Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His	
275 280 285	
ATG CTG TCA CAG ACC AAA CAG GGT GGG GAG AAT TTC CCA TAC CTT GTA	912
Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro Tyr Leu Val	
290 295 300	
GCG TAC CAA GCA ACA GTC TGT GTT CGC GCG AAA GCG CCC CCC CCC AGC	960
Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser	
305 310 315 320	
TGG GAC ACA ATG TGG AAA TGC ATG CTC CGT CTC AAA CCG ACT TTA ACT	1008
Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr	
325 330 335	
GGC CCT ACT CCC CTC TTG TAC AGG CTG GGG CCC GTC CAG AAT GAG ATC	1056
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile	
340 345 350	
ACA CTG ACG CAC CCC ATC ACC AAG TAC ATT ATG GCT TGC ATG TCT GCG	1104
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	
355 360 365	
GAC TTG GAG GTC ATT ACC AGC ACT TGG GTT CTG GTG GGG GGC GTT GTG	1152
Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val	
370 375 380	
GCG GCC CTG GCG GCC TAC TGC TTG ACG GTG GGT TCG GTA GCC ATA GTC	1200
Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val	
385 390 395 400	
GGT AGG ATC ATC CTC TCT GGG AAA CCT GCC ATC ATT CCC GAT AGG GAG	1248
Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu	
405 410 415	
GCA TTA TAC CAG CAA TTT GAT GAG ATG GAG GAG TGC TCG GCC TCG TTG	1296
Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu	
420 425 430	
CCC TAT ATG GAC GAG ACA CGT GCC ATT GCC GGA CAA TTC AAA GAG AAA	1344
Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys	
435 440 445	
GTG CTC GGC TTC ATC AGC ACG ACC GGC CAG AAG GCT GAA ACT CTG AAG	1392
Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys	
450 455 460	
CCG GCA GCC ACG TCT GTG TGG AAC AAG GCT GAG CAG TTC TGG GCC ACA	1440
Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr	
465 470 475 480	



TAC  
Tyr

1443

## (2) INFORMATION FOR SEQ ID NO: 270:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

Thr Ile Thr Thr Gly Ala Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe  
 1 5 10 15

Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Val Ile Ile Cys  
 20 25 30

Asp Glu Cys His Ser Gln Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr  
 35 40 45

Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala  
 50 55 60

Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn Ile Glu  
 65 70 75 80

Glu Val Ala Leu Pro Gln Glu Gly Glu Val Pro Phe Tyr Gly Arg Ala  
 85 90 95

Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu Ile Phe Cys His  
 100 105 110

Ser Lys Lys Lys Cys Asp Glu Leu Ala Lys Gln Leu Thr Ser Leu Gly  
 115 120 125

Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ala Val Ile Pro  
 130 135 140

Thr Ala Gly Asp Val Val Val Cys Ser Thr Asp Ala Leu Met Thr Gly  
 145 150 155 160

Phe Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Ser Ala Val Thr  
 165 170 175

Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr  
 180 185 190

Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr  
 195 200 205

Gly Arg Gly Arg His Gly Ile Tyr Arg Tyr Val Ser Ala Gly Glu Arg  
 210 215 220

Pro Ser Asp Met Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala

225	230	235	240
Gly Cys Ala Trp Tyr Asp Leu Thr Pro Ala Glu Thr Thr Val Arg Leu	245	250	255
Arg Ala Tyr Ile Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu	260	265	270
Glu Phe Trp Glu Gly Val Phe Thr Gly Leu Thr Asn Ile Asp Ala His	275	280	285
Met Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Pro Tyr Leu Val	290	295	300
Ala Tyr Gln Ala Thr Val Cys Val Arg Ala Lys Ala Pro Pro Pro Ser	305	310	315
Trp Asp Thr Met Trp Lys Cys Met Leu Arg Leu Lys Pro Thr Leu Thr	325	330	335
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Pro Val Gln Asn Glu Ile	340	345	350
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	355	360	365
Asp Leu Glu Val Ile Thr Ser Thr Trp Val Leu Val Gly Gly Val Val	370	375	380
Ala Ala Leu Ala Ala Tyr Cys Leu Thr Val Gly Ser Val Ala Ile Val	385	390	395
Gly Arg Ile Ile Leu Ser Gly Lys Pro Ala Ile Ile Pro Asp Arg Glu	405	410	415
Ala Leu Tyr Gln Gln Phe Asp Glu Met Glu Glu Cys Ser Ala Ser Leu	420	425	430
Pro Tyr Met Asp Glu Thr Arg Ala Ile Ala Gly Gln Phe Lys Glu Lys	435	440	445
Val Leu Gly Phe Ile Ser Thr Thr Gly Gln Lys Ala Glu Thr Leu Lys	450	455	460
Pro Ala Ala Thr Ser Val Trp Asn Lys Ala Glu Gln Phe Trp Ala Thr	465	470	475
Tyr			480

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